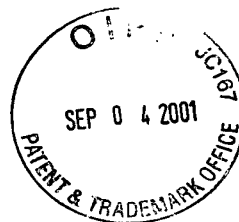


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24737-1906C

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Edward T. Maggio
P. Patrick Hess

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Structures of Genetic Polymorphisms in Pharmacogenomics for
Drug Design and Clinical Applications

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TECH CENTER 1600/2900

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Peptide

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 <222> (1)...(297)
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<221> CDS
 <222> (298)...(1045)
 <223> Portion of Reverse Transcriptase

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ggc caa cta aaa gaa gct yta tta gat aca gga gca gat gat aca gta	96
Gly Gln Leu Lys Glu Ala Xaa Leu Asp Thr Gly Ala Asp Asp Thr Val	
20 25 30	
tta gaa gaa atg agt tta cca ggg aaa tgg aaa cca aaa atg ata ggg	144
Leu Glu Glu Met Ser Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly	
35 40 45	
gga att gga ggt ttt atc aaa gta aga cag tat gat caa ata ctc ata	192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Leu Ile	
50 55 60	
gaa atc tgt gga cat aaa gct ata ggc aca gta tta gta gga cct aca	240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr	
65 70 75 80	

cct gtc aac ata att gga aga aat ttg ttg act cag att ggt tgc act	288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr	
85 90 95	
tta aat ttg ccc att agt cct att gaa act gta cca gta aaa tta aag	336
Leu Asn Leu Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys	
100 105 110	
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa	384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu	
115 120 125	
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa gga	432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly	
130 135 140	
aaa att tca aaa att ggg cct gag aat cca tac aat act cca ata ttt	480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe	
145 150 155 160	
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc	528
Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe	
165 170 175	
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Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly	
180 185 190	
ata cca cac ccc gca ggg tta aaa cag aaa aaa tca gta aca ata ctg	624
Ile Pro His Pro Ala Gly Leu Lys Gln Lys Lys Ser Val Thr Ile Leu	
195 200 205	
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat gaa ggc ttc agg	672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Gly Phe Arg	
210 215 220	
aag tat act gca ttt acc ata cct agt aga aat aat gag aca cca ggg	720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Arg Asn Asn Glu Thr Pro Gly	
225 230 235 240	
att aga tat cag tac aac gtg ctc cca cag gga tgg aaa gga tca cca	768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro	
245 250 255	
gca ata ttt caa agt agc atg aca aga aty tta gag cct ttt aga aaa	816
Ala Ile Phe Gln Ser Ser Met Thr Arg Xaa Leu Glu Pro Phe Arg Lys	
260 265 270	
caa aat cca gaa ata gtt atc tat caa tac atg gat gat ttg tat gta	864
Gln Asn Pro Glu Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val	
275 280 285	
gga tct gac tta gaa ata gga cag cat aga gca aaa ata gag gaa ctg	912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Leu	
290 295 300	
aga gga cat cta tta aag tgg gga ttt acc aca cca gac aaa aaa cat	960
Arg Gly His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His	
305 310 315 320	
cag aaa gaa cct cca ttt ctt tgg atg ggt tat gaa ctc cat cct gat	1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp	
325 330 335	

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 <211> 1046
 <212> DNA
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 <221> CDS
 <222> (1)...(297)
 <223> HIV Protease

<221> CDS
 <222> (298)...(1046)
 <223> Portion of HIV Reverse Transcriptase

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 ggg cag cta aag gaa gct cta tta gat aca gga gca gat gat aca gta 96
 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Thr Val
 20 25 30
 gtt gaa gaa atg aat ttg cca gga aaa tgg aaa cca aaa atg ata ggg 144
 Val Glu Glu Met Asn Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly
 35 40 45
 gga att gga ggt ttt atc aaa gta aga cag tat gag caa ata gcc gta 192
 Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Glu Gln Ile Ala Val
 50 55 60
 gaa aty tgt gga cat aga gct atg ggt aca gta tta gta gga cct aca 240
 Glu Xaa Cys Gly His Arg Ala Met Gly Thr Val Leu Val Gly Pro Thr
 65 70 75 80
 cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act 288
 Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
 85 90 95
 tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
 100 105 110
 cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
 115 120 125
 aaa ata aaa gca tta gta gaa atc tgt aca gaa ttg gaa aag gaa ggg 432
 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly
 130 135 140
 aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt 480
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
 145 150 155 160
 gcc ata aag aaa aag aac agt act aaa tgg aga aaa tta gta gat ttc 528
 Ala Ile Lys Lys Lys Asn Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
 165 170 175


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      180                      185                      190

ata cca cat cca gca ggg tta aaa aag aat aaa tca ata aca gta ctg      624
Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Ile Thr Val Leu
      195                      200                      205

gat gtg ggt gat gca tat ttt tca gtt ccc tta tgt gaa gac ttc agg      672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Cys Glu Asp Phe Arg
      210                      215                      220

aag tat act gca ttt acc ata cct agt gta aac aat gag act cca ggg      720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Val Asn Asn Glu Thr Pro Gly
      225                      230                      235                      240

att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga ttc acc      768
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      245                      250                      255

agc ata ttc caa tgt agc atg aca aaa atc tta gag cct ttt aga aaa      816
Ser Ile Phe Gln Cys Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys
      260                      265                      270

caa aat cca gag ata gtt atc tat caa tac atg gat gat ttg tat gta      864
Gln Asn Pro Glu Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val
      275                      280                      285

gga tct gac tta gaa ata ggg cag cat aga gca aaa ata gag gaa ctg      912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Leu
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cag aaa gaa cct cct ttc ctt tgg atg ggt tat gaa ctc cat ccc gat      1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
      325                      330                      335

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<210> 5
<211> 1104
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

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<221> CDS
<222> (1) ... (297)
<223> HIV Protease

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<221> CDS
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<223> Portion of HIV Reverse Transcriptase

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      1                      5                      10                      15

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ata gaa gac ata act ttg cca gga aga tgg aca cca aaa atg ata ggg Ile Glu Asp Ile Thr Leu Pro Gly Arg Trp Thr Pro Lys Met Ile Gly 35 40 45	144
gga att gga ggt ttt gtc aaa gta aga cag tat gat cag ata ccc ata Gly Ile Gly Gly Phe Val Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile 50 55 60	192
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cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aag gca tta gta gaa att tgt mca gaa ctg gaa atg gat gga Lys Ile Lys Ala Leu Val Glu Ile Cys Xaa Glu Leu Glu Met Asp Gly 130 135 140	432
aaa att tca aaa att ggg cct gaa aat ccg tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gcc ata aag aaa aag aac agt act aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asn Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528
aga gaa ctt aac aaa aga act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat ccc gca ggg tta aag aag aaa aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu 195 200 205	624
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 275 280 285

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 Gly Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Asp Glu Leu
 290 295 300

aga caa tat ctg tgg aag tgg gga ttt tac aca cca gac aaa aaa cat 960
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 305 310 315 320

cag aca gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat 1008
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 325 330 335

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 340 345 350

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<223> HIV Protease

<221> CDS

<222> (298)...(1116)

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ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta 96
 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
 20 25 30

tta gaa gat atg aat ttg cca gga aga tgg aaa cca aaa atg ata ggg 144
 Leu Glu Asp Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
 35 40 45

gga att gga ggt ttt atc aaa gta agg cag tat gat caa ata ctc ata 192
 Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Leu Ile
 50 55 60

gaa atc tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca 240
 Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr
 65 70 75 80

cct gtc aac ata att gga agg aat ctg ttg act cag att ggt tgc act 288
 Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
 85 90 95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gag gag Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
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aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528
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ata cca cat ccc gca ggg tta aaa aag aaa aag tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu 195 200 205	624
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gga tct gac tta gaa ata gga cag cac aga aca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300	912
aga caa cat ctg ttg aag tgg gga ttt acc aca cca gac aag aaa cat Arg Gln His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His 305 310 315 320	960
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
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Ile Tyr Pro Gly
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<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

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      1                      5                      10                      15

ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
      20                      25                      30

tta gag gaa atn aat tta cca gga aga tgg aaa cca aaa atg ata ggg      144
Leu Glu Glu Xaa Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
      35                      40                      45

gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ctt gta      192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Leu Val
      50                      55                      60

gaa aty tgt gga cat aar gct ata ggt aca gta tta gta gga cct aca      240
Glu Xaa Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr
      65                      70                      75                      80

ccc gtc aac ata att gga aga aat ctg ttg act caa att ggt tgc act      288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
      85                      90                      95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag      336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
      100                      105                      110

ccg gga atg gat ggc ccc aaa gtt aaa cat ggc cct ttg aca gaa gaa      384
Pro Gly Met Asp Gly Pro Lys Val Lys His Gly Pro Leu Thr Glu Glu
      115                      120                      125

aaa ata aag cct tta gtt gaa att tgt aca gaa atg gga aaa gaa ggg      432
Lys Ile Lys Pro Leu Val Glu Ile Cys Thr Glu Met Gly Lys Glu Gly
      130                      135                      140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt      480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
      145                      150                      155                      160

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165 170 175

aga gaa ctt aat aaa aga act caa gac tty tgg gaa gtc caa tta gga 576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
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ata cca cat ccc tca ggg tta aaa aag aaa aaa tca gta aca gta ctg 624
Ile Pro His Pro Ser Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu
195 200 205

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210 215 220

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Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly
225 230 235 240

att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca 768
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245 250 255

gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa 816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys
260 265 270

caa aat cca gac ata gtt atc tat caa tac atg gat gat ttg tat gta 864
Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val
275 280 285

gga tca gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg 912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu
290 295 300

aga caa cat ctg ttg ggg tgg ggg ttt acc aca cca gac aaa aaa cat 960
Arg Gln His Leu Leu Gly Trp Gly Phe Thr Thr Pro Asp Lys Lys His
305 310 315 320

cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat 1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
325 330 335

aaa tgg aca gta cag cct ata gtg ctg cca aca aaa gac agc tgg act 1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Thr Lys Asp Ser Trp Thr
340 345 350

gtc aat gac ata cag aag tta gtg gga aaa ttg aac tgg gca agt cag 1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
355 360 365

att tat gca ggg
Ile Tyr Ala Gly 1116
370

<210> 8

<211> 1116

<212> DNA

<213> Human Immunodeficiency Virus (HIV)

<220>

<221> CDS
 <222> (1)...(297)
 <223> HIV Protease

<221> CDS
 <222> (298)...(1116)
 <223> Portion of HIV Reverse Transcriptase

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<400> 8
cct cag atc act ctt tgg caa cga ccc cty gtc aca gta aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Xaa Val Thr Val Lys Ile Gly
  1                    5                    10                    15

ggg caa ata aag gaa gct yta tta gat aca gga gca gat gat aca gta      96
Gly Gln Ile Lys Glu Ala Xaa Leu Asp Thr Gly Ala Asp Asp Thr Val
                    20                    25                    30

tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa ata ata ggg      144
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Ile Ile Gly
                    35                    40                    45

gga att gga ggt ttt atc aaa gta aga cag tat gat cag gta ccc ata      192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Val Pro Ile
                    50                    55                    60

gaa atc tgt gga caa aaa gct ata agt aca gta tta gta gga cct aca      240
Glu Ile Cys Gly Gln Lys Ala Ile Ser Thr Val Leu Val Gly Pro Thr
  65                    70                    75                    80

cct gtc aat ata att gga aga aat ctg atg act cag att ggt tgc act      288
Pro Val Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Ile Gly Cys Thr
                    85                    90                    95

tta aat ttt cct att agt cct att gaa act gta cca gta aaa tta aag      336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
                    100                    105                    110

cca gga atg gat ggc cca aga gtt aaa caa tgg cca ttg aca gaa gaa      384
Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu
                    115                    120                    125

aaa ata aaa gca tta gta gaa atc tgt aca gaa atg gaa aag gaa ggg      432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
                    130                    135                    140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt      480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
                    145                    150                    155                    160

gcc ata aag aaa aaa ggc agt aac aga tgg aga aaa tta gta gat ttc      528
Ala Ile Lys Lys Lys Gly Ser Asn Arg Trp Arg Lys Leu Val Asp Phe
                    165                    170                    175

aga gaa ctt aat aag aaa act caa gac ttc tgg gaa gtt caa tta gga      576
Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
                    180                    185                    190

ata cca cat ccc gca ggg cta aaa aag aaa aaa tca gta aca gta ctg      624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu
                    195                    200                    205

gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gaa ttc agg      672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Glu Phe Arg
                    210                    215                    220

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aag tat act gca ttt acc ata cct agt aca aac aat gag aca cca ggg      720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly
225                               230                               235                               240

att aga tat cag tac aat gtg ctt cca caa gga tgg aaa ggg tca cca      768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
                               245                               250                               255

gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa      816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys
                               260                               265                               270

caa aat cca gac ata gtt atc tat caa tac atg gat gat ttg tat gta      864
Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val
                               275                               280                               285

agc tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa cta      912
Ser Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu
                               290                               295                               300

aga caa cat ctg ttg agg tgg gga tta acc aca cca gac aaa aaa cat      960
Arg Gln His Leu Leu Arg Trp Gly Leu Thr Thr Pro Asp Lys Lys His
305                               310                               315                               320

cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat      1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
                               325                               330                               335

aaa tgg aca gta cag cct ata gtg ctg cca gar aaa gac agc tgg act      1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
                               340                               345                               350

gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt caa      1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
                               355                               360                               365

att tac cca ggg
Ile Tyr Pro Gly
370

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<210> 9
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

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<400> 9
cct cag atc act ctt tgg caa cga ccc cty gtc aaa gta aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Xaa Val Lys Val Lys Ile Gly
1                               5                               10                               15

ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
                               20                               25                               30

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tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atg ata ggg Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly 35 40 45	144
gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ccc ata Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile 50 55 60	192
gaa atc tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr 65 70 75 80	240
cct gtc aac ata atw gga aga aat ctg ttg act cag att ggt tgc act Pro Val Asn Ile Xaa Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr 85 90 95	288
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta ata gaa att tgt aca gag atg gag aag gaa ggg Lys Ile Lys Ala Leu Ile Glu Ile Cys Thr Glu Met Glu Lys Glu Gly 130 135 140	432
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528
aga gaa ctt aat aag aaa act caa gay ttc tgg gaa gtt car tta gga Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg 210 215 220	672
aag tat act gca ttt acc ata cct agt gta aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Val Asn Asn Glu Thr Pro Gly 225 230 235 240	720
att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agt agc atg aca aag atc tta gar cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gaa ata gtt atc tat caa tac atg gat gat ttg tat gta Gln Asn Pro Glu Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864

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gga tcw gac tta gaa ata ggg caa cat aga ata aaa ata gag gaa ctg      912
Gly Xaa Asp Leu Glu Ile Gly Gln His Arg Ile Lys Ile Glu Glu Leu
290                               295                               300

aga cag cat ctg tta agg tgg ggg ttt acc aca cca gac aaa aaa cat      960
Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His
305                               310                               315                               320

cag aaa gaa cct cca ttc ctt tgg atg ggk tat gaa ctc cat cct gat      1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Xaa Tyr Glu Leu His Pro Asp
325                               330                               335

aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gay agc tgg act      1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
340                               345                               350

gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag      1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
355                               360                               365

atc tac cca ggg
Ile Tyr Pro Gly
370

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<210> 10
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

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<400> 10
cct cag atc act ctt tgg caa cga ccc ctc gtc aca gta aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Val Lys Ile Gly
1                               5                               10                               15

ggg caa ata aag gaa gct yta tta gat aca gga gca gat gat aca gta      96
Gly Gln Ile Lys Glu Ala Xaa Leu Asp Thr Gly Ala Asp Asp Thr Val
20                               25                               30

tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atw ata ggg      144
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Xaa Ile Gly
35                               40                               45

gga att gga ggt ttt atc aaa gta aga cag tat gat cag gta ccc ata      192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Val Pro Ile
50                               55                               60

gaa atc tgt gga caa aaa gct ata agt aca gta tta gta gga cct aca      240
Glu Ile Cys Gly Gln Lys Ala Ile Ser Thr Val Leu Val Gly Pro Thr
65                               70                               75                               80

cct gtc aat ata att gga aga aat ctg atg act cag att ggt tgc act      288
Pro Val Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Ile Gly Cys Thr
85                               90                               95

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tta aat ttt cct att agt cct att gaa act gta cca gta aaa taa aag	336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys * Lys	
100 105 110	
cca gga atg gat ggc cca aga gtt aaa caa tgg cca ttg aca gaa gaa	384
Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu	
115 120 125	
aaa ata aaa gca tta gta gaa atc tgt aca gaa atg gaa aag gaa ggg	432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly	
130 135 140	
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt	480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe	
145 150 155	
gcc ata aag aaa aaa ggc agt aac aga tgg aga aaa tta gta gat ttc	528
Ala Ile Lys Lys Lys Gly Ser Asn Arg Trp Arg Lys Leu Val Asp Phe	
160 165 170 175	
aga gaa ctt aat aag aaa act caa gac ttc tgg gaa gtt caa tta gga	576
Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Gly	
180 185 190	
ata cca cat ccc gca ggg cta aaa aag aaa aaa tca gta aca gta ctg	624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu	
195 200 205	
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gaa ttc agg	672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Glu Phe Arg	
210 215 220	
aag tat act gca ttt acc ata cct agt aca aac aat gag aca cca ggg	720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly	
225 230 235	
att aga tat cag tac aat gtg ctt ccm caa gga tgg aaa ggg tca cca	768
Ile Arg Tyr Gln Tyr Asn Val Leu Xaa Gln Gly Trp Lys Gly Ser Pro	
240 245 250 255	
gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa	816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys	
260 265 270	
caa aat cca gac wtr gtt atc tat caa tac atg gat gat ttg tat gta	864
Gln Asn Pro Asp Xaa Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val	
275 280 285	
agc tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa cta	912
Ser Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu	
290 295 300	
aga caa cat ctg ttg agg tgg gga tta acc aca cca gac aaa aaa cat	960
Arg Gln His Leu Leu Arg Trp Gly Leu Thr Thr Pro Asp Lys Lys His	
305 310 315	
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat	1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp	
320 325 330 335	
aaa tgg aca gta cag cct ata gtg ctg cca gag aaa gac agc tgg act	1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr	
340 345 350	

gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt caa 1104
 Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
 355 360 365

att tac cca ggg 1116
 ile tyr pro gly
 370

<210> 11
 <211> 1116
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)

<220>
 <221> CDS
 <222> (1)...(297)
 <223> HIV Protease

<221> CDS
 <222> (298)...(1116)
 <223> Portion of HIV Reverse Transcriptase

<400> 11
 cct cag atc act ctt tgg caa cga ccc aty gtt aca ata aag ata ggg 48
 Pro Gln ile Thr Leu Trp Gln Arg Pro Xaa Val Thr ile Lys ile Gly
 1 5 10 15

ggg caa cta aaa raa gct cta tta gat aca gga gca gat gat aca gta 96
 Gly Gln Leu Lys Xaa Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
 20 25 30

tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atg ata gtg 144
 Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met ile Val
 35 40 45

gga att gga ggt ttt gtc aaa gta aga cag tat gat cag gta ccc ata 192
 Gly ile Gly Gly Phe Val Lys Val Arg Gln Tyr Asp Gln Val Pro ile
 50 55 60

gag atc tgt ggg cat aaa att ata ggt aca gta tta ata gga cct acc 240
 Glu ile Cys Gly His Lys ile ile Gly Thr Val Leu ile Gly Pro Thr
 65 70 75 80

cct gcc aac gta att gga aga aat ctg atg act cag ctt ggt tgc act 288
 Pro Ala Asn Val ile Gly Arg Asn Leu Met Thr Gln Leu Gly Cys Thr
 85 90 95

tta aat ttt ccc att agt yct att gaa act gta cca gta aaa tta aag 336
 Leu Asn Phe Pro ile Ser Xaa ile Glu Thr Val Pro Val Lys Leu Lys
 100 105 110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
 115 120 125

aaa ata aaa gca tta gta gaa att tgt gca gaa ctg gag aag gaa ggg 432
 Lys ile Lys Ala Leu Val Glu ile Cys Ala Glu Leu Glu Lys Glu Gly
 130 135 140

aaa att tca aga att ggg cct gaa aat cca tac aat act cca ata ttt 480
 Lys ile Ser Arg ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro ile Phe
 145 150 155 160

gcc ata aag aag aaa aac agt act agg tgg aga aaa tta gta gat ttc 528
 Ala Ile Lys Lys Lys Asn Ser Thr Arg Trp Arg Lys Leu Val Asp Phe
 165 170 175

aga gaa ctt aat aag aga act caa gac ttc tgg gaa att caa tta gga 576
 Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Ile Gln Leu Gly
 180 185 190

ata cca cat cct gca ggg tta aaa aag aac aaa tca gta aca gta ctg 624
 Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu
 195 200 205

gat gtg ggg gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg 672
 Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg
 210 215 220

aag tac act gca ttt acc ata cct agt aca aac aat gag aca cca ggg 720
 Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly
 225 230 235 240

att aga tat cag tac aat gtg ctt cca caa gga tgg aaa gga tca cca 768
 Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
 245 250 255

gca ata ttc caa gat agc atg aca aaa atc tta gat ccc ttt aga aag 816
 Ala Ile Phe Gln Asp Ser Met Thr Lys Ile Leu Asp Pro Phe Arg Lys
 260 265 270

aaa aat cca gac ata gtt atc tat caa tac gtg gat gat ttg tat gta 864
 Lys Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val
 275 280 285

gga tct gac yta gaa ata gag cag cat aga gca aaa ata gag gaa ctg 912
 Gly Ser Asp Xaa Glu Ile Glu Gln His Arg Ala Lys Ile Glu Glu Leu
 290 295 300

aga gaa tat ctg tta aag tgg gga ttt ttc aca cca gag caa aaa cat 960
 Arg Glu Tyr Leu Leu Lys Trp Gly Phe Phe Thr Pro Glu Gln Lys His
 305 310 315 320

cag aaa gaa cct cca ttc ctt tgg atg ggc tat gaa ctc cat cct gat 1008
 Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
 325 330 335

aaa tgg aca gtg cag cct ata gtg ctg cca gaa aag gac agc tgg act 1056
 Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
 340 345 350

gtc aat gac ata cag aag tta gtg gga aaa ttg aac tgg gca agt cag 1104
 Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
 355 360 365

att tac cca ggg
 Ile Tyr Pro Gly 1116
 370

<210> 12

<211> 1116

<212> DNA

<213> Human Immunodeficiency Virus (HIV)

<220>

<221> CDS
 <222> (1)...(297)
 <223> HIV Protease

<221> CDS
 <222> (298)...(1116)
 <223> Portion of HIV Reverse Transcriptase

<400> 12

cct	caa	atc	act	ctt	tgg	car	cga	ccc	tta	gtc	aca	ata	aag	ata	ggg	48
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1				5					10					15		
ggg	caa	cta	aag	gaa	gcc	cta	tta	gat	aca	gga	gca	gat	gat	aca	gta	96
Gly	Gln	Leu	Lys	Glu	Ala	Leu	Leu	Asp	Thr	Gly	Ala	Asp	Asp	Thr	Val	
			20					25					30			
cta	gaa	gaa	atg	aat	ttg	cca	gga	aaa	tgg	aaa	cca	aaa	atg	ata	ggg	144
Leu	Glu	Glu	Met	Asn	Leu	Pro	Gly	Lys	Trp	Lys	Pro	Lys	Met	Ile	Gly	
			35				40					45				
gga	att	gga	ggg	ttt	atc	aaa	gta	agg	cag	tat	gat	car	ata	ccc	ata	192
Gly	Ile	Gly	Gly	Phe	Ile	Lys	Val	Arg	Gln	Tyr	Asp	Gln	Ile	Pro	Ile	
	50					55					60					
gag	atc	tgc	ggg	tat	aaa	gct	gtg	ggg	aca	gta	tta	gta	gga	cct	aca	240
Glu	Ile	Cys	Gly	Tyr	Lys	Ala	Val	Gly	Thr	Val	Leu	Val	Gly	Pro	Thr	
	65				70					75					80	
cct	gtc	aac	ata	att	gga	aga	aat	ctg	ttg	act	caa	att	ggg	tgc	act	288
Pro	Val	Asn	Ile	Ile	Gly	Arg	Asn	Leu	Leu	Thr	Gln	Ile	Gly	Cys	Thr	
				85					90					95		
tta	aat	ttt	ccc	att	agt	cct	att	gaa	act	gta	cca	gta	aaa	tta	aag	336
Leu	Asn	Phe	Pro	Ile	Ser	Pro	Ile	Glu	Thr	Val	Pro	Val	Lys	Leu	Lys	
			100					105					110			
cca	gga	atg	gat	ggc	cca	aaa	gtt	aaa	caa	tgg	cca	ttg	aca	gaa	gaa	384
Pro	Gly	Met	Asp	Gly	Pro	Lys	Val	Lys	Gln	Trp	Pro	Leu	Thr	Glu	Glu	
		115					120					125				
aaa	ata	aaa	gca	tta	ata	gaa	att	tgt	aca	gaa	atg	gaa	aag	gaa	gga	432
Lys	Ile	Lys	Ala	Leu	Ile	Glu	Ile	Cys	Thr	Glu	Met	Glu	Lys	Glu	Gly	
	130					135					140					
aaa	att	tca	aaa	att	ggg	cct	gaa	aat	cca	tac	aat	act	cca	gta	ttt	480
Lys	Ile	Ser	Lys	Ile	Gly	Pro	Glu	Asn	Pro	Tyr	Asn	Thr	Pro	Val	Phe	
	145				150				155						160	
gcc	ata	aag	aaa	aaa	gac	ggg	act	aaa	tgg	aga	aaa	tta	gta	gat	ttc	528
Ala	Ile	Lys	Lys	Lys	Asp	Gly	Thr	Lys	Trp	Arg	Lys	Leu	Val	Asp	Phe	
				165					170					175		
aga	gaa	ctt	aat	aag	aga	act	caa	gac	ttc	tgg	gaa	gtt	caa	tta	gga	576
Arg	Glu	Leu	Asn	Lys	Arg	Thr	Gln	Asp	Phe	Trp	Glu	Val	Gln	Leu	Gly	
			180					185					190			
ata	cca	cat	ccc	gca	ggg	tta	aaa	aag	aaa	aaa	tca	gta	aca	gta	cta	624
Ile	Pro	His	Pro	Ala	Gly	Leu	Lys	Lys	Lys	Lys	Ser	Val	Thr	Val	Leu	
			195				200					205				
gat	gtg	ggg	gat	gca	tat	ttt	tca	gtt	ccc	tta	gat	caa	gac	ttc	aga	672
Asp	Val	Gly	Asp	Ala	Tyr	Phe	Ser	Val	Pro	Leu	Asp	Gln	Asp	Phe	Arg	
	210					215					220					

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aag tat act gca ttc act ata cct agt ata aac aat gag aca cca ggg      720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly
225                230                235                240

att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca      768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
                245                250                255

gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa      816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys
                260                265                270

caa aat cca gac atg gtt atc tat caa tat atg gat gat ttg tat gta      864
Gln Asn Pro Asp Met Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val
                275                280                285

ggc tct gac tta gaa aya ggg cag cat aga rca aaa ata gag gaa ctg      912
Gly Ser Asp Leu Glu Xaa Gly Gln His Arg Xaa Lys Ile Glu Glu Leu
290                295                300

aga caa cat ctg ttg agg tgg gga ttt acc aca cca gac aaa aaa cat      960
Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His
305                310                315                320

cag aaa gaa cct cca ttt ctt tgg atg ggt tat gaa ctc cat cct gat     1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
                325                330                335

aaa tgg aca gta cag cct ata atg ctg cca gaa aaa gac agc tgg act     1056
Lys Trp Thr Val Gln Pro Ile Met Leu Pro Glu Lys Asp Ser Trp Thr
                340                345                350

gtc aat gac ata cag aag cta gtg gga aaa ttg aat tgg gca agt cag     1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
                355                360                365

att tat gca ggg
Ile Tyr Ala Gly
370
1116

<210> 13
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

<400> 13
cct cag atc act ctt tgg caa cga ccc aty gtc aac ata aag gta ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Xaa Val Asn Ile Lys Val Gly
1                5                10                15

ggg caa cta arg gaa gct cta ata gat aca gga gca gat gat aca gta      96
Gly Gln Leu Xaa Glu Ala Leu Ile Asp Thr Gly Ala Asp Asp Thr Val
                20                25                30

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tta gaa gac Leu Glu Asp	ata gat Ile Asp	ttg cca Leu Pro	gga aga Gly Arg	tgg aga Trp Arg	cca aga Pro Arg	atg ata Met Ile	ggg Gly	144
35			40		45			
gga att gga Gly Ile Gly	ggt ttt Gly Phe	gtc aaa Val Lys	gta aag Val Lys	cag tat Gln Tyr	gat cag Asp Gln	ata ccc Ile Pro	ata Ile	192
50		55			60			
gaa ata tgt Glu Ile Cys	gga cat Gly His	aaa gtt Lys Val	ata ggt Ile Gly	aca gta Thr Val	tta gta Leu Val	gga cct Gly Pro	acg Thr	240
65		70		75			80	
cct gcc aac Pro Ala Asn	ata att Ile Ile	gga aga Gly Arg	aat ctg Asn Leu	ttg act Leu Thr	cag att Gln Ile	ggg tgc Gly Cys	act Thr	288
	85			90		95		
tta aat ttt Leu Asn Phe	ccc att Pro Ile	agt cct Ser Pro	att gaa Ile Glu	act gta Thr Val	cca gta Pro Val	aaa tta Lys Leu	aaa Lys	336
	100		105			110		
cca gga atg Pro Gly Met	gat ggc Asp Gly	cca aaa Pro Lys	gtt aaa Val Lys	caa tgg Gln Trp	cca ttg Pro Leu	aca gaa Thr Glu	gaa Glu	384
115			120		125			
aag ata aaa Lys Ile Lys	gca tta Ala Leu	gta gaa Val Glu	att tgt Ile Cys	aca gaa Thr Glu	ttg gaa Leu Glu	aag gaa Lys Glu	gga Gly	432
130		135			140			
aaa att tca Lys Ile Ser	aaa att Lys Ile	ggg cct Gly Pro	gaa aat Glu Asn	cca tac Pro Tyr	aat act Asn Thr	cca gta Pro Val	ttt Phe	480
145		150		155			160	
gcc ata aag Ala Ile Lys	aag aag Lys Lys	aaa aac Lys Asn	agt act Ser Thr	aga tgg Arg Trp	aga aaa Arg Lys	tta gta Leu Val	gat ttt Asp Phe	528
	165			170			175	
aga gaa ctt Arg Glu Leu	aat aag Asn Lys	aga act Arg Thr	caa gac Gln Asp	ttt tgt Phe Cys	gaa gtg Glu Val	caa tta Gln Leu	gga Gly	576
	180		185			190		
ata ccg cat Ile Pro His	ccc gca Pro Ala	ggg tta Gly Leu	ara aag Xaa Lys	aaa aga Lys Arg	tca gta Ser Val	aca gta Thr Val	ctg Leu	624
195			200		205			
gat gtg ggt Asp Val Gly	gat gca Asp Ala	tat ttt Tyr Phe	tca gtt Ser Val	ccc tta Pro Leu	gat gaa Asp Glu	gac ttc Asp Phe	agg Arg	672
210		215			220			
aag tat act Lys Tyr Thr	gcc ttt Ala Phe	acc ata Thr Ile	cct agt Pro Ser	ata aac Ile Asn	aat gag Asn Glu	aca cca Thr Pro	ggg Gly	720
225		230		235			240	
att aga tat Ile Arg Tyr	cag tat Gln Tyr	aat gtg Asn Val	ctt cca Leu Pro	cag gga Gln Gly	tgg aaa Trp Lys	gga tca Gly Ser	cca Pro	768
	245			250		255		
gca ata ttc Ala Ile Phe	caa agt Gln Ser	agc atg Ser Met	aca aaa Thr Lys	atc cta Ile Leu	gag cct Glu Pro	ttt aga Phe Arg	aaa Lys	816
	260		265			270		
caa aat cca Gln Asn Pro	grc ata Xaa Ile	gtt atc Val Ile	gtt caa Val Gln	tac gtg Tyr Val	gat gat Asp Asp	ttg tat Leu Tyr	gta Val	864
	275		280		285			


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ggg tct gac tta gaa ata ggg caa cat aga gca aaa ata gag gag ttg      912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Leu
290                295                300

aga gaa cat ctg ttg agg tgg gga tty ttc aca cca gac gaa aaa cat      960
Arg Glu His Leu Leu Arg Trp Gly Phe Phe Thr Pro Asp Glu Lys His
305                310                315                320

cag aaa gaa cct cca ttt ctt tgg atg ggt tat gaa ctc cac cct gat      1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
325                330                335

aaa tgg acc gta cag cct ata aat ttg cca gaa aaa gac agc tgg act      1056
Lys Trp Thr Val Gln Pro Ile Asn Leu Pro Glu Lys Asp Ser Trp Thr
340                345                350

gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag      1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
355                360                365

att tac tca ggg
Ile Tyr Ser Gly
370

<210> 14
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

<400> 14
cct caa atc act ctt tgg caa cga ccc ctc gtc aca ata aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly
1                5                10                15

ggg caa gta agg gaa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Val Arg Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
20                25                30

tta gaa gaa atg aat ttg cca gga aaa tgg aag cca aaa atg ata ggg      144
Leu Glu Glu Met Asn Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly
35                40                45

gga att ggg ggc ttt atc aaa gta aga cag tat gat caa ata ccc ata      192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile
50                55                60

gaa atc tgt gga cat aaa gct ata ggg aca gtg tta ata gga cct aca      240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Ile Gly Pro Thr
65                70                75                80

cct gtc aac ata att gga aga aat ctg ttg act cag ctt ggt tgc act      288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr
85                90                95

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tta aat ttt cct att agt cct att gaa act gtg cca gta aaa tta aag	336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys	
100 105 110	
cca gga atg gat ggt cca aaa gtt aaa caa tgg cca ttg aca gaa gaa	384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu	
115 120 125	
aaa ata aaa gca ttg ata gaa att tgt aca gaa atg gaa aag gaa gga	432
Lys Ile Lys Ala Leu Ile Glu Ile Cys Thr Glu Met Glu Lys Glu Gly	
130 135 140	
aag att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt	480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe	
145 150 155 160	
gcc ata aag aaa aaa aac agt act aga tgg agg aaa cta gta gac ttc	528
Ala Ile Lys Lys Lys Asn Ser Thr Arg Trp Arg Lys Leu Val Asp Phe	
165 170 175	
aga gaa ctt aat aag aga act caa gac ttt tgg gaa gtt caa tta gga	576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly	
180 185 190	
ata cca cat ccc gca gga tta aaa aag aga aaa tca gta aca gta ctg	624
Ile Pro His Pro Ala Gly Leu Lys Lys Arg Lys Ser Val Thr Val Leu	
195 200 205	
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aar gac ttc agg	672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg	
210 215 220	
aaa tac act gca ttc acc ata cct agt ata aac aat gag aca cca ggg	720
Lys Tyr Thr Ala Phe Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly	
225 230 235 240	
att aga tat cag tac aat gtg ctg cca caa gga tgg aaa gga tca cca	768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro	
245 250 255	
tca ata ttc caa agt agy atg aca aaa atc tta gag cct ttt aga aag	816
Ser Ile Phe Gln Ser Xaa Met Thr Lys Ile Leu Glu Pro Phe Arg Lys	
260 265 270	
caa aat cca gac ata gat atc tgt caa tac atg gat gat ttg tat gta	864
Gln Asn Pro Asp Ile Asp Ile Cys Gln Tyr Met Asp Asp Leu Tyr Val	
275 280 285	
gga tct gac tta gaa ata ggg cag cat aga gca aaa ata rag gaa ctg	912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Xaa Glu Leu	
290 295 300	
aga gag cat ctg cta aag tgg gga ttt acc aca cca gac raa aaa cat	960
Arg Glu His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Xaa Lys His	
305 310 315 320	
car aaa gaa cct cca ttt ctt tgg atg ggt tat gaa ctt cat cct gat	1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp	
325 330 335	
aaa tgg aca gta caa cat ata gag cta cca gaa aaa gac agc tgg act	1056
Lys Trp Thr Val Gln His Ile Glu Leu Pro Glu Lys Asp Ser Trp Thr	
340 345 350	

gtc aat gac ata caa aag tta gtg gga aaa tta aat tgg gca agt cag 1104
 Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
 355 360 365

att tat gca ggg 1116
 Ile Tyr Ala Gly
 370

<210> 15
 <211> 1116
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)

<220>
 <221> CDS
 <222> (1)...(297)
 <223> HIV Protease

 <221> CDS
 <222> (298)...(1116)
 <223> Portion of HIV Reverse Transcriptase

<400> 15
 cct caa atc act ctt tgg car cga ccc ctc gtt gca ata aag ata ggg 48
 Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Ala Ile Lys Ile Gly
 1 5 10 15

ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta 96
 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
 20 25 30

tta kaa gaa atg gat ttg cca gga aga tgg aaa cca aaa atg ata ggg 144
 Leu Xaa Glu Met Asp Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
 35 40 45

gga att gga ggt ttt atc aaa gta aga cag tat gat cag gta tcc wta 192
 Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Val Ser Xaa
 50 55 60

gaa atc tgt gga cat aaa gct ata ggt aca gta tta ata gga cct aca 240
 Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Ile Gly Pro Thr
 65 70 75 80

cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act 288
 Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
 85 90 95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
 100 105 110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
 115 120 125

aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa gga 432
 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
 130 135 140

aaa att tca aaa att ggg cct gaa aat cca tat aat act cca gta ttt 480
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
 145 150 155 160

gcc ata aag aaa aaa gac agt act aaa tgg aga aaa ttg gta gat ttc 528
Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
165 170 175

aga gaa ctt aat aag aaa act caa gac ttc tgg gar gtt caa tta gga 576
Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
180 185 190

ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta ctg 624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu
195 200 205

gat gtg ggt gat gca tat ttt tca gtt ccc tta gat cca gac ttc agg 672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Pro Asp Phe Arg
210 215 220

aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca gga 720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly
225 230 235 240

atc aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca 768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
245 250 255

gca ata ttt caa agy agc atg ata aga aty tta gag cct ttt aga aaa 816
Ala Ile Phe Gln Xaa Ser Met Ile Arg Xaa Leu Glu Pro Phe Arg Lys
260 265 270

caa aat cca gaa ata gtt atc tat caa tac atg gat gat ttg tat gta 864
Gln Asn Pro Glu Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val
275 280 285

gga tct gat tta gaa ata gaa cag cat aga gca aaa ata gag gaa ctg 912
Gly Ser Asp Leu Glu Ile Glu Gln His Arg Ala Lys Ile Glu Glu Leu
290 295 300

aga caa cat ctg tta agg tgg gga ttt acc aca cca gay aaa aaa cat 960
Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His
305 310 315 320

cag aaa gaa cct cca ttc ctt tgg atg gga tat gaa ctc cat cct gat 1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Xaa Tyr Glu Leu His Pro Asp
325 330 335

aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act 1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
340 345 350

gtc aat gac ata cag aag ttr gtg gga aaa ttr aat tgg gca agt cag 1104
Val Asn Asp Ile Gln Lys Xaa Val Gly Lys Xaa Asn Trp Ala Ser Gln
355 360 365

att tac tca ggg 1116
Ile Tyr Ser Gly
370

<210> 16
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)
<220>

<221> CDS
 <222> (1)...(297)
 <223> HIV Protease

<221> CDS
 <222> (298)...(1116)
 <223> Portion of HIV Reverse Transcriptase

<400> 16
 cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata aag ata ggg 48
 Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly
 1 5 10 15

ggg caa cta aag gag gct cta tta gat aca gga gca gat gat aca gta 96
 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
 20 25 30

tta gaa gac atg act ttg cca gga aga tgg aaa cca aaa atg ata ggg 144
 Leu Glu Asp Met Thr Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
 35 40 45

gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ccc ata 192
 Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile
 50 55 60

gaa atc tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca 240
 Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr
 65 70 75 80

cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act 288
 Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
 85 90 95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
 100 105 110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
 115 120 125

aaa ata aaa gca tta rta gaa att tgt aca gaa atg gaa aag gaa gga 432
 Lys Ile Lys Ala Leu Xaa Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
 130 135 140

aag att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt 480
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
 145 150 155 160

gcc ata aag aaa aar gat ggt act aaa tgg aga aaa tta gta gat ttc 528
 Ala Ile Lys Lys Lys Asp Gly Thr Lys Trp Arg Lys Leu Val Asp Phe
 165 170 175

aga gaa ctt aat aag aga act caa gac ttc tgg gaa att caa tta gga 576
 Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Ile Gln Leu Gly
 180 185 190

ata cca cat cct gca ggg tta aaa aag aaa aag tca gta aca gta ctg 624
 Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu
 195 200 205

gat gtg ggt gat gca tat ttt tca gtt ccc tta gat gaa gac ttc agg 672
 Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg
 210 215 220

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aag tat act gca ttt act ata cct agt ata aac aat gag aca cca ggg      720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly
225                               230                               235                               240

att aga tat cag tac aat gtg ctt cca caa gga tgg aaa gga tca cca      768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
                               245                               250                               255

gca ata ttc caa tgt agc atg aca aaa atc tta gag cct ttt aga aag      816
Ala Ile Phe Gln Cys Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys
                               260                               265                               270

caa aat cca gac ata gtt atc tat caa tac atg gat gat ttg tat gta      864
Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val
                               275                               280                               285

gga tct gac tta gaa ata ggg cag cat aga rca aaa ata gag gaa ctg      912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Xaa Lys Ile Glu Glu Leu
                               290                               295                               300

agg caa cat ctg ttg aag tgg gga ttt acc aca cca gac aaa aaa cat      960
Arg Gln His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His
305                               310                               315                               320

cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cca gat     1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
                               325                               330                               335

aaa tgg aca gta cag cct ata gtg ctg cca caa aaa gac agc tgg act     1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Gln Lys Asp Ser Trp Thr
                               340                               345                               350

gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag     1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
                               355                               360                               365

att tat cca ggg
Ile Tyr Pro Gly
                               370

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<210> 17
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

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<220>
<221> CDS
<222> (1) ... (297)
<223> HIV Protease

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<221> CDS
<222> (298) ... (1116)
<223> Portion of HIV Reverse Transcriptase

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<400> 17
cct caa atc act ctt tgg caa cga ccc aty gtc aca ata aag gta ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Xaa Val Thr Ile Lys Val Gly
1                               5                               10                               15

ggg caa cta aag gaa gcc cta ata gat aca gga gca gat gat aca gtg      96
Gly Gln Leu Lys Glu Ala Leu Ile Asp Thr Gly Ala Asp Asp Thr Val
                               20                               25                               30

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tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa ttg ata ggg Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Leu Ile Gly 35 40 45	144
gga att gga ggt ttt atc aaa gta aga cag tat gat cag rta ccc ata Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Xaa Pro Ile 50 55 60	192
gaa atc tgt gga cat aaa gct gta ggt tca gtg tta gta gga cct aca Glu Ile Cys Gly His Lys Ala Val Gly Ser Val Leu Val Gly Pro Thr 65 70 75 80	240
cct gcc aac ata att gga aga aat ctg ttg act cag att ggt tgc act Pro Ala Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr 85 90 95	288
cta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca aaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Lys Glu 115 120 125	384
aaa ata gaa gca tta gta gaa atc tgt gca gaa ctg gaa gag gca ggg Lys Ile Glu Ala Leu Val Glu Ile Cys Ala Glu Leu Glu Ala Gly 130 135 140	432
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gcc ata aag aar aag aac agt act aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asn Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528
aga gaa ctt aac aag aga act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttc tca att ccc tta gat aag gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Ile Pro Leu Asp Lys Asp Phe Arg 210 215 220	672
aag tat act gca ttt aca ata cct agy ata aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Xaa Ile Asn Asn Glu Thr Pro Gly 225 230 235 240	720
att aga tat cag tac aat gtg ctt cma cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Xaa Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc cag tgt agc atg aca aaa atc tta gat cct ttt aga aaa Ala Ile Phe Gln Cys Ser Met Thr Lys Ile Leu Asp Pro Phe Arg Lys 260 265 270	816
caa aat cca gac ata gtt atc tat caa tac gtg gat gat ttg tat gta Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val 275 280 285	864

gga tct gac tta gaa ata ggg car cat aga aca aaa ata gag gaa ctg 912
 Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu
 290 295 300

aga caa yat ctg tgg aag tgg gga ttt tac aca cca gag aat aaa cat 960
 Arg Gln Xaa Leu Trp Lys Trp Gly Phe Tyr Thr Pro Glu Asn Lys His
 305 310 315 320

cag aaa gaa cct cca ttc cwt tgg atg ggt tat gaa ctc cat cct gat 1008
 Gln Lys Glu Pro Pro Phe Xaa Trp Met Gly Tyr Glu Leu His Pro Asp
 325 330 335

aaa tgg aca gta cag cct ata gtg ctg cca gaa aag gac agc tgg act 1056
 Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
 340 345 350

gtc aat gac ata cag aaa tta gtg gga aaa ttg aat tgg gca agt cag 1104
 Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
 355 360 365

att tat gcn ggg 1116
 Ile Tyr Ala Gly
 370

<210> 18
 <211> 1117
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)

<220>
 <221> CDS
 <222> (1)...(297)
 <223> HIV Protease

<221> CDS
 <222> (298)...(1117)
 <223> Portion of HIV Reverse Transcriptase

<400> 18
 cct caa atc act ctt tgg caa cga ccc ctc gtc aca ata aag ata ggg 48
 Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly
 1 5 10 15

ggg car cta aag gaa gct cta tta gat aca gga gca gat gat aca gta 96
 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
 20 25 30

gta gaa gaa atg aat tta tca gga agg tgg aaa cca aaa atg ata ggg 144
 Val Glu Glu Met Asn Leu Ser Gly Arg Trp Lys Pro Lys Met Ile Gly
 35 40 45

gga att gga ggt ttt atc aaa gta aga saa tat gaa cag ata cct gta 192
 Gly Ile Gly Gly Phe Ile Lys Val Arg Xaa Tyr Glu Gln Ile Pro Val
 50 55 60

gaa att tgt gga cat aaa gct gta ggt aca gta tta gtg gga cct aca 240
 Glu Ile Cys Gly His Lys Ala Val Gly Thr Val Leu Val Gly Pro Thr
 65 70 75 80

cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act 288
 Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
 85 90 95

tta aat ttt ccc att agt ccc att gaa act gta cca gta aaa ttg aag	336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys	
100 105 110	
cca gga atg gat ggc ccg aga gtt aaa caa tgg cca ttg aca gaa gaa	384
Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu	
115 120 125	
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa ggg	432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly	
130 135 140	
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt	480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe	
145 150 155 160	
gcc ata aag aaa aaa gac agt aat aaa tgg agg aaa tta gtg gat ttc	528
Ala Ile Lys Lys Lys Asp Ser Asn Lys Trp Arg Lys Leu Val Asp Phe	
165 170 175	
aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta ggg	576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly	
180 185 190	
ata cca cat ccy tca ggg tta aaa aag aaa aaa tca gta aca gta ctg	624
Ile Pro His Xaa Ser Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu	
195 200 205	
gat gtg ggt gat gca tac ttt tca gtt ccc tta gat aaa gaa ttc agg	672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Glu Phe Arg	
210 215 220	
aag tat act gca ttt acc ata cct agt aca aac aat gag aca cca ggg	720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly	
225 230 235 240	
att agr tat cag tac aat gtg ctg cca cag gga tgg aaa gga tca cca	768
Ile Xaa Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro	
245 250 255	
gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga gaa	816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Glu	
260 265 270	
caa aat aca gac ata gtt atc tgt caa tac atg gat gat ttg tat gta	864
Gln Asn Thr Asp Ile Val Ile Cys Gln Tyr Met Asp Asp Leu Tyr Val	
275 280 285	
gga tct gac tta gaa ata ggg cag cat aga gca aaa gtr gag gaa ctg	912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Xaa Glu Glu Leu	
290 295 300	
aga caa cat ctg ttg agg tgg gga yta acc aca cca gac aaa aaa cat	960
Arg Gln His Leu Leu Arg Trp Gly Xaa Thr Thr Pro Asp Lys Lys His	
305 310 315 320	
cag aaa gaa cct cca ttc cgt tgg atg ggk tat gaa ctc cat cct gat	1008
Gln Lys Glu Pro Pro Phe Arg Trp Met Xaa Tyr Glu Leu His Pro Asp	
325 330 335	
aaa tgg aca gtr caa cct ata gag ctg cca gaa aaa gac agc tgg act	1056
Lys Trp Thr Xaa Gln Pro Ile Glu Leu Pro Glu Lys Asp Ser Trp Thr	
340 345 350	

gtc aat gac ata caa aaa gtt agt ggg aaa att aaa ttg ggc aag tca 1104
 Val Asn Asp Ile Gln Lys Val Ser Gly Lys Ile Lys Leu Gly Lys Ser
 355 360 365

gat tta ccc agg g 1117
 Asp Leu Pro Arg
 370

<210> 19
 <211> 1116
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)

<220>
 <221> CDS
 <222> (1) ... (297)
 <223> HIV Protease

<221> CDS
 <222> (298) ... (1116)
 <223> Portion of HIV Reverse Transcriptase

<400> 19
 cct cag atc act ctt tgg caa cga ccc cty gtc aca gta aag ata ggg 48
 Pro Gln Ile Thr Leu Trp Gln Arg Pro Xaa Val Thr Val Lys Ile Gly
 1 5 10 15

ggg caa cta acg gaa gct yta ttg gat aca gga gca gat aat aca gta 96
 Gly Gln Leu Thr Glu Ala Xaa Leu Asp Thr Gly Ala Asp Asn Thr Val
 20 25 30

tta gaa gaa atg agt ttr cca gga aga tgg aaa cca aaa atg ata ggg 144
 Leu Glu Glu Met Ser Xaa Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
 35 40 45

gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ccc ata 192
 Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile
 50 55 60

gaa atc tgt gga cat aaa gta gta ggt aca gta tta ata gga cct aca 240
 Glu Ile Cys Gly His Lys Val Val Gly Thr Val Leu Ile Gly Pro Thr
 65 70 75 80

cct gtc aac ata att gga aga gat ctg ttg act cag att ggt tgc act 288
 Pro Val Asn Ile Ile Gly Arg Asp Leu Leu Thr Gln Ile Gly Cys Thr
 85 90 95

tta aat ttt ccc att agt cct att gaa act gta cca gtg aaa tta aag 336
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
 100 105 110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
 115 120 125

aaa ata aaa gca tta gta gaa att tgt aca gaa ctg gaa aag gaa ggg 432
 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly
 130 135 140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt 480
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
 145 150 155 160

gcc ata aag aaa aar gac agt act aaa tgg aga aaa ttr gta gat ttc 528
Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Xaa Val Asp Phe
165 170 175

aga gaa ctt aat aaa aga act caa gac ttc tgg gaa gtt caa tta gga 576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
180 185 190

ata cca cat ccc tca ggg tta aaa aag aaa aaa tca gta aca gta cta 624
Ile Pro His Pro Ser Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu
195 200 205

gac gtg ggt gat gca tat ttc tca gtt ccc cta gat aaa gaa ttc agg 672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Glu Phe Arg
210 215 220

aag tat act gca ttc acc ata cct agt gta aac aat gag act cca ggg 720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Val Asn Asn Glu Thr Pro Gly
225 230 235 240

att aga tat cag tac aat gtg ctg cca cag gga tgg aaa gga tca cca 768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
245 250 255

gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa 816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys
260 265 270

cac aat cca aac ata gtt atc tat caa tac gtg gat gat tta tat gta 864
His Asn Pro Asn Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val
275 280 285

gga tct gac tta gaa ata ggg cag cat aga aca aaa gta gag gaa ctg 912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Val Glu Glu Leu
290 295 300

aga caa cat ctg ttg aag tgg ggg ttt tac aca cca gac aaa aaa cat 960
Arg Gln His Leu Leu Lys Trp Gly Phe Tyr Thr Pro Asp Lys Lys His
305 310 315 320

cag aaa gaa ccc cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat 1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
325 330 335

aaa tgg aca gtg cag cct ata gtg ctg cca gaa aaa gac agc tgg act 1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
340 345 350

gtc aat gac ata caa aag tta gtg gga aaa ttg aat tgg gca agt cag 1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
355 360 365

att tac cca ggg
Ile Tyr Pro Gly 1116
370

<210> 20
<211> 1117
<212> DNA
<213> Human Immunodeficiency Virus (HIV)
<220>

<221> CDS
 <222> (1)...(297)
 <223> HIV Protease

<221> CDS
 <222> (298)...(1117)
 <223> Portion of HIV Reverse Transcriptase

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<400> 20
cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata aag ata gga      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly
  1             5             10             15

ggg cag cta aag gaa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
             20             25             30

tta gaa gac ata aat ttg cca ggg aaa tgg aaa cca aaa atg ata ggg      144
Leu Glu Asp Ile Asn Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly
             35             40             45

gga att gga ggt ttt atc aaa gta aga cag tat gat caa ata cca gta      192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Val
  50             55             60

gaa att tgt gga cat aaa gct gta ggt aca gta tta ata gga cct aca      240
Glu Ile Cys Gly His Lys Ala Val Gly Thr Val Leu Ile Gly Pro Thr
  65             70             75             80

cct gtc aac gta att gga aga aat ctg atg act cag att ggc tgc act      288
Pro Val Asn Val Ile Gly Arg Asn Leu Met Thr Gln Ile Gly Cys Thr
             85             90             95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag      336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
             100            105            110

cca gga atg gat ggt cca aaa gtt aaa caa tgg cca tta aca gaa gaa      384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
             115            120            125

aaa ata aaa gca tta gta gaa att tgc aca gaa ttg gaa aag gaa ggg      432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly
             130            135            140

aaa att tca aaa att gga cct gaa aat cca tac aat act cca gta ttt      480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
             145            150            155            160

gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc      528
Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
             165            170            175

aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga      576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
             180            185            190

ata cca cat cct gca ggg tta aaa aag aaa aaa tca gta aca gta ctg      624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu
             195            200            205

gat gtg ggt gat gca tat ttt tca ata ccc tta gat gaa gaa ttc agg      672
Asp Val Gly Asp Ala Tyr Phe Ser Ile Pro Leu Asp Glu Glu Phe Arg
             210            215            220

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aag tat act gca ttt acc ata cct agt cca aac aat gag aca cca ggg      720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Pro Asn Asn Glu Thr Pro Gly
225                               230                               235                               240

att aga tat caa tac aat gtg ctt cca cag gga tgg aaa gga tca cca      768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
                               245                               250                               255

gca ata ttt caa tgt agt atg aca aaa atc tta gag cct ttt aga aaa      816
Ala Ile Phe Gln Cys Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys
                               260                               265                               270

gaa aat cca gat ata gtt atc tac caa tac atg gat gac tta tat gta      864
Glu Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val
                               275                               280                               285

gga tct gat tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg      912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu
290                               295                               300

aga caa tat ctg tgg aag tgg gga ttt tac aca cca gac aaa aaa cat      960
Arg Gln Tyr Leu Trp Lys Trp Gly Phe Tyr Thr Pro Asp Lys Lys His
305                               310                               315                               320

cag caa gaa cct cca ttc cgt tgg atg ggt tat gaa ctc cat cct gat      1008
Gln Gln Glu Pro Pro Phe Arg Trp Met Gly Tyr Glu Leu His Pro Asp
                               325                               330                               335

aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act      1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
                               340                               345                               350

gtc aat gac ata cag aag ttt agt ggg aaa att gaa ttg ggc aag tca      1104
Val Asn Asp Ile Gln Lys Phe Ser Gly Lys Ile Glu Leu Gly Lys Ser
355                               360                               365

gat tta tgc agg g
Asp Leu Cys Arg
370

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<210> 21
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

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<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

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<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

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<400> 21
cct cag atc act ctt tgg caa cga mcc gtt gtc wca ata aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Xaa Val Val Xaa Ile Lys Ile Gly
1                               5                               10                               15

ggg caa cta aaa gaa gct cta tta gay aca ggg gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
20                               25                               30

```

tta gaa gac atg cat ttg cca ggt aga tgg aaa cca aaa atg ata gtg Leu Glu Asp Met His Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Val 35 40 45	144
gga att ggg ggt ttt gtc aaa gta aga cag tat gat cag ata cct gta Gly Ile Gly Gly Phe Val Lys Val Arg Gln Tyr Asp Gln Ile Pro Val 50 55 60	192
gaa atc tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr 65 70 75 80	240
cca gcc aac ata att gga aga aat ctg ttg act cag att ggt tgc act Pro Ala Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr 85 90 95	288
tta aat ttc ccc atc agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa att aga caa tgg cca tta aca gaa gaa Pro Gly Met Asp Gly Pro Lys Ile Arg Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta gta gaa atc tgt aca gaa atg gaa aag gaa ggg Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly 130 135 140	432
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gcc ata aag aaa aaa aat agt act aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asn Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528
aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta cta Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg 210 215 220	672
aag tat act gca ttt acc ata cct agt atg aac aat gag aca cca gga Lys Tyr Thr Ala Phe Thr Ile Pro Ser Met Asn Asn Glu Thr Pro Gly 225 230 235 240	720
att aga tat cag tac aat gtg ctt cca atg gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Met Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agt agt atg aca aaa atc tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
cag aat cca gac ata gtc atc tat caa tac atg gat gat tta tat gta Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864

gga tcg gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ttg 912
 Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu
 290 295 300

aga caa cat ctg ttg aga tgg gga ttt acc aca cca gac aaa aaa cat 960
 Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His
 305 310 315 320

cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat 1008
 Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
 325 330 335

aaa tgg aca gtg cag cct ata gtg ctg cca gaa aag gac agc tgg act 1056
 Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
 340 345 350

gtt aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt caa 1104
 Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
 355 360 365

att tat gca ggg 1116
 Ile Tyr Ala Gly
 370

<210> 22
 <211> 1116
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)

<220>
 <221> CDS
 <222> (1)...(297)
 <223> HIV Protease

<221> CDS
 <222> (298)...(1116)
 <223> Portion of HIV Reverse Transcriptase

<400> 22
 cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata aag gta gga 48
 Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Val Gly
 1 5 10 15

ggg caa cta aag gag gct cta tta gat aca gga gca gat gat aca gta 96
 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
 20 25 30

tta gaa gac ata gat ttg cca gga agr tgg aaa cca aaa atg ata ggg 144
 Leu Glu Asp Ile Asp Leu Pro Gly Xaa Trp Lys Pro Lys Met Ile Gly
 35 40 45

gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ccc ata 192
 Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile
 50 55 60

gaa ata tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca 240
 Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr
 65 70 75 80

cct gtc aac ata att gga aga aat ctg ttg act cgg att ggt tgc act 288
 Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Arg Ile Gly Cys Thr
 85 90 95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag	336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys	
100 105 110	
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa	384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu	
115 120 125	
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa gga	432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly	
130 135 140	
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt	480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe	
145 150 155 160	
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttt	528
Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe	
165 170 175	
aga gaa ctt aat aag aga act caa gat ttc tgg gaa gtg caa tta gga	576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly	
180 185 190	
ata ccg cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta ctg	624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu	
195 200 205	
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aar gay ttc agg	672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg	
210 215 220	
aag tat act gcc ttt acc ata cct agt ata aac aat gag aca cca ggg	720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly	
225 230 235 240	
att aga tat cag tat aat gtg ctt cca cag gga tgg aaa gga tca cca	768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro	
245 250 255	
gca ata ttc caa agt agc atg aca aaa atc cta gag cct ttt aga aaa	816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys	
260 265 270	
caa aat cca gac atg gtt atc tat caa tac atg gat gat ttg tat gta	864
Gln Asn Pro Asp Met Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val	
275 280 285	
ggg tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg	912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu	
290 295 300	
aga gaa cat ctg ttg agg tgg gga ttt acc acc cca gac aaa aaa cat	960
Arg Glu His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His	
305 310 315 320	
cag aaa gag cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat	1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp	
325 330 335	
aaa tgg acc gtr cag cct ata gag ctg cca gaa aaa gac agc tgg act	1056
Lys Trp Thr Xaa Gln Pro Ile Glu Leu Pro Glu Lys Asp Ser Trp Thr	
340 345 350	


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gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag      1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
      355                      360                      365

att tac cca ggg      1116
Ile Tyr Pro Gly
      370

<210> 23
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

<400> 23
cct cag atc act ctt tgg caa cga ccc ata gtc aca ata aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Ile Gly
      1                      5                      10                      15

ggg caa cta aag gaa gct cta ata gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Ile Asp Thr Gly Ala Asp Asp Thr Val
      20                      25                      30

tta gaa gac ata aat ttg cca gga aga tgg aaa cca aaa tta ata ggg      144
Leu Glu Asp Ile Asn Leu Pro Gly Arg Trp Lys Pro Lys Leu Ile Gly
      35                      40                      45

gga att gga ggt ttt gtc aga gtg aaa cag tat gat cag ata ccc ata      192
Gly Ile Gly Gly Phe Val Arg Val Lys Gln Tyr Asp Gln Ile Pro Ile
      50                      55                      60

gaa att tgt gga cat aaa gtt ata ggt aca gta tta gta gga cct aca      240
Glu Ile Cys Gly His Lys Val Ile Gly Thr Val Leu Val Gly Pro Thr
      65                      70                      75                      80

cct gcc aac ata att gga aga aat ctg ttg act cag att ggt tgc act      288
Pro Ala Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
      85                      90                      95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag      336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
      100                     105                     110

cca gga atg gat ggc cca aga gtt aaa caa tgg cca ttg aca gaa gaa      384
Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu
      115                     120                     125

aaa ata aaa gca tta aca gaa atc tgt wca gag atg gaa aag gaa ggg      432
Lys Ile Lys Ala Leu Thr Glu Ile Cys Xaa Glu Met Glu Lys Glu Gly
      130                     135                     140

aaa att tca aaa att ggg cct gaa aat cca tac aac act cca gta ttt      480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
      145                     150                     155                     160

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gcy ata cac aag aaa aat agt aat aga tgg aga aaa gta gta gat ttc Xaa Ile His Lys Lys Asn Ser Asn Arg Trp Arg Lys Val Val Asp Phe 165 170 175	528
agg gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat ccc gca gga tta aaa aag aac aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aag gat ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg 210 215 220	672
aag tat act gcg ttt acc ata cct agt ata aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240	720
atc aga tac cag tac aat gtg ctt cca caa gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agt agc atg aca aga atc tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Arg Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gaa ata gtt atc tgt caa tac atg gat gat ttg tat gta Gln Asn Pro Glu Ile Val Ile Cys Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac tta gaa ata ggg cag cat aga aca aaa ata aak gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Xaa Glu Leu 290 295 300	912
aga saa cat ctg ttg agg tgg gga ttt ttc aca cca gac caa aaa cat Arg Xaa His Leu Leu Arg Trp Gly Phe Phe Thr Pro Asp Gln Lys His 305 310 315 320	960
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta cag cct ata gtg ctg cca gaa aar gac agt tgg acw Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Xaa 340 345 350	1056
gty aat gac ata cag aaa tta gtk gga aaa ttg aat tgg gca agt caa Xaa Asn Asp Ile Gln Lys Leu Xaa Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
att tac cca ggg Ile Tyr Pro Gly 370	1116

<210> 24

<211> 1116

<212> DNA

<213> Human Immunodeficiency Virus (HIV)

<220>

<221> CDS
 <222> (1)...(297)
 <223> HIV Protease

<221> CDS
 <222> (298)...(1116)
 <223> Portion of HIV Reverse Transcriptase

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<400> 24
cct cag atc act ctt tgg caa cga ccc ata gtc aca ata aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Ile Gly
  1                               10                               15

ggg caa cta aag gaa gct cta ata gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Ile Asp Thr Gly Ala Asp Asp Thr Val
                20                               25                               30

tta gaa gac ata aat ttg cca gga aga tgg aaa cca aaa tta ata ggg      144
Leu Glu Asp Ile Asn Leu Pro Gly Arg Trp Lys Pro Lys Leu Ile Gly
                35                               40                               45

gga att gga ggt ttt gtc aga gtg aaa cag tat gat cag ata ccc ata      192
Gly Ile Gly Gly Phe Val Arg Val Lys Gln Tyr Asp Gln Ile Pro Ile
                50                               55                               60

gaa att tgt gga cat aaa gtt ata ggt aca gta tta gta gga cct aca      240
Glu Ile Cys Gly His Lys Val Ile Gly Thr Val Leu Val Gly Pro Thr
                65                               70                               75

cct gcc aac ata att gga aga aat ctg ttg act cag att ggt tgc act      288
Pro Ala Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
                85                               90                               95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag      336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
                100                              105                              110

cca gga atg gat ggc cca aga gtt aaa caa tgg cca ttg aca gaa gaa      384
Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu
                115                              120                              125

aaa ata aaa gca tta aca gaa atc tgt wca gag atg gaa aag gaa ggg      432
Lys Ile Lys Ala Leu Thr Glu Ile Cys Xaa Glu Met Glu Lys Glu Gly
                130                              135                              140

aaa att tca aaa att ggg cct gaa aat cca tac aac act cca gta ttt      480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
                145                              150                              155

gcy ata cac aag aaa aat agt aat aga tgg aga aaa gta gta gat ttc      528
Xaa Ile His Lys Lys Asn Ser Asn Arg Trp Arg Lys Val Val Asp Phe
                165                              170                              175

agg gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga      576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
                180                              185                              190

ata cca cat ccc gca gga tta aaa aag aac aaa tca gta aca gta ctg      624
Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu
                195                              200                              205

gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aag gat ttc agg      672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg
                210                              215                              220

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aag tat act gcg ttt acc ata cct agt ata aac aat gag aca cca ggg      720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly
225                               230                               235                               240

atc aga tac cag tac aat gtg ctt cca caa gga tgg aaa gga tca cca      768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
                               245                               250                               255

gca ata ttc caa agt agc atg aca aga atc tta gag cct ttt aga aaa      816
Ala Ile Phe Gln Ser Ser Met Thr Arg Ile Leu Glu Pro Phe Arg Lys
                               260                               265                               270

caa aat cca gaa ata gtt atc tgt caa tac atg gat gat ttg tat gta      864
Gln Asn Pro Glu Ile Val Ile Cys Gln Tyr Met Asp Asp Leu Tyr Val
                               275                               280                               285

gga tct gac tta gaa ata ggg cag cat aga aca aaa ata aak gaa ctg      912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Xaa Glu Leu
                               290                               295                               300

aga saa cat ctg ttg agg tgg gga ttt ttc aca cca gac caa aaa cat      960
Arg Xaa His Leu Leu Arg Trp Gly Phe Phe Thr Pro Asp Gln Lys His
305                               310                               315                               320

cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat      1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
                               325                               330                               335

aaa tgg aca gta cag cct ata gtg ctg cca gaa aar gac agt tgg acw      1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Xaa
                               340                               345                               350

gty aat gac ata cag aaa tta gtk gga aaa ttg aat tgg gca agt caa      1104
Xaa Asn Asp Ile Gln Lys Leu Xaa Gly Lys Leu Asn Trp Ala Ser Gln
                               355                               360                               365

att tac cca ggg
Ile Tyr Pro Gly
                               370

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<210> 25
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

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<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

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<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

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<400> 25
cct caa atc act ctt tgg caa cga ccc ctc gtc aca ata aaa ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly
1                               5                               10                               15

ggg caa cta aag gaa gct cta cta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
                               20                               25                               30

```

tta gaa gaa atg agt ttg cca gga aaa tgg aaa cca aaa atg ata ggg Leu Glu Glu Met Ser Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly 35 40 45	144
gga att gga ggt ttt atc aaa gta aga cag tat gat cag gta tcc atg Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Val Ser Met 50 55 60	192
gaa atc tgt gga cat aaa gtt ata ggt aca gta tta gta gga tct aca Glu Ile Cys Gly His Lys Val Ile Gly Thr Val Leu Val Gly Ser Thr 65 70 75 80	240
cct gtc aac ata att gga aga aat ytg ttg act cag ctt ggg tgc act Pro Val Asn Ile Ile Gly Arg Asn Xaa Leu Thr Gln Leu Gly Cys Thr 85 90 95	288
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta ata gaa att tgt aca gaa atg gaa aag gar ggg Lys Ile Lys Ala Leu Ile Glu Ile Cys Thr Glu Met Glu Lys Glu Gly 130 135 140	432
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gcc ata aag aaa aaa gac agt act aaa tgg aga aag tta gta gat ttc Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528
aga gaa ctt aat aag aaa act caa gat ttc tgg gaa rtt caa tta gga Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Xaa Gln Leu Gly 180 185 190	576
ata cca cat ccc gca ggg tta caa aag aac aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Gln Lys Asn Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtc ccc tta gat aaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg 210 215 220	672
aag tat act gca ttt acc ata cct agt aca aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly 225 230 235 240	720
att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa tat agc atg aca aaa atc tta gag cct ttt aga aaa Ala Ile Phe Gln Tyr Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gac ata gtt atc tac caa tac gtg gat gat ttg tat gta Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val 275 280 285	864

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gga tct gac tta gaa ata gaa cag cat aga aca aaa ata gag gaa ctg      912
Gly Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Glu Glu Leu
290                               295                               300

aga cag cat ctg ttg agg tgg gga ttt acc aca cca gac aaa aaa cat      960
Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His
305                               310                               315                               320

cag aaa gaa cct cca ttc ctc tgg atg ggt tat gaa ctc cat cct gat      1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
325                               330                               335

aaa tgg aca gtt cag cct ata gtg ctg cca gaa aag gac agc tgg act      1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
340                               345                               350

gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt cag      1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
355                               360                               365

att tac cca ggg
Ile Tyr Pro Gly
370

<210> 26
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

<400> 26
cct cag atc act ctt tgg caa cga ccc atc gtc gaa ata aag gta ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Glu Ile Lys Val Gly
1                               5                               10                               15

ggg caa cta ata gaa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Ile Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
20                               25                               30

tta gaa gaa ata aat tta cca gga aga tgg aaa cca aga atg ata ggg      144
Leu Glu Glu Ile Asn Leu Pro Gly Arg Trp Lys Pro Arg Met Ile Gly
35                               40                               45

gga att gga ggt ttt gtc aaa gta aga cag tat gat cag gta cct atc      192
Gly Ile Gly Gly Phe Val Lys Val Arg Gln Tyr Asp Gln Val Pro Ile
50                               55                               60

gaa atc tgt gga cat aaa gtt ata agt aca gta tta gta gga cct aca      240
Glu Ile Cys Gly His Lys Val Ile Ser Thr Val Leu Val Gly Pro Thr
65                               70                               75                               80

cct gcc aac ata att gga aga aat ctg atg act cag att ggt tgc act      288
Pro Ala Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Ile Gly Cys Thr
85                               90                               95

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tta aat ttt cct att agt cct att gaa act gta cca gta aaa tta aaa	336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys	
100 105 110	
cca gga atg gat ggc cca aga gtt aaa caa tgg cca ttg aca gaa gaa	384
Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu	
115 120 125	
aaa ata aaa gca tta gta gaa att tgt aca gaa ytg gaa gag gaa ggg	432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Xaa Glu Glu Glu Gly	
130 135 140	
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca ata ttt	480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe	
145 150 155 160	
gcc ata aag aag aaa nnn agt ggt aga tgg aga aaa ata gta gat ttt	528
Ala Ile Lys Lys Lys Xaa Ser Gly Arg Trp Arg Lys Ile Val Asp Phe	
165 170 175	
aga gaa ctt aat aag aga act caa gat ttc tgg gaa gtt caa tta gga	576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly	
180 185 190	
ata cca cat ccc gca ggg tta aaa aag aac aag tca gta aca att ctg	624
Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Ile Leu	
195 200 205	
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aag gaa ttc agg	672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Glu Phe Arg	
210 215 220	
aag tat act gca ttt acc ata cct agt ata aat aat gag aca cca ggg	720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly	
225 230 235 240	
att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca	768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro	
245 250 255	
gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa	816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys	
260 265 270	
caa aat cca gac ata gtt atc tat cag tac gtg gat gat ttg tat gta	864
Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val	
275 280 285	
gga tct gat tta gaa ata ggg gag cat aga aca aaa ata gag gaa ctg	912
Gly Ser Asp Leu Glu Ile Gly Glu His Arg Thr Lys Ile Glu Glu Leu	
290 295 300	
aga car cat ctg tta arg tgg gga ttt ttc aca cca gaa caa aaa cat	960
Arg Gln His Leu Leu Xaa Trp Gly Phe Phe Thr Pro Glu Gln Lys His	
305 310 315 320	
cag aaa gaa cct ccm ttc cak tgg atg ggt tat gaa ctc cay cct gat	1008
Gln Lys Glu Pro Xaa Phe Xaa Trp Met Gly Tyr Glu Leu His Pro Asp	
325 330 335	
aaa tgg aca gta cas cct ata gtg ctg cca gaa aaa gat agc tgg act	1056
Lys Trp Thr Val Xaa Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr	
340 345 350	

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gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag      1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
      355                      360                      365

att tac cca ggg      1116
Ile Tyr Pro Gly
      370

<210> 27
<211> 1113
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

<400> 27
cct cag atc act ctt tgg caa cga ccc atc gtc gaa ata aag gta ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Glu Ile Lys Val Gly
      1                      5                      10                      15

ggg caa cta ata gaa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Ile Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
      20                      25                      30

tta gaa gaa ata aat tta cca gga aga tgg aaa cca aga atg ata ggg      144
Leu Glu Glu Ile Asn Leu Pro Gly Arg Trp Lys Pro Arg Met Ile Gly
      35                      40                      45

gga att gga ggt ttt gtc aaa gta aga cag tat gat cag gta cct atc      192
Gly Ile Gly Gly Phe Val Lys Val Arg Gln Tyr Asp Gln Val Pro Ile
      50                      55                      60

gaa atc tgt gga cat aaa gtt ata agt aca gta tta gta gga cct aca      240
Glu Ile Cys Gly His Lys Val Ile Ser Thr Val Leu Val Gly Pro Thr
      65                      70                      75                      80

cct gcc aac ata att gga aga aat ctg atg act cag att ggt tgc act      288
Pro Ala Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Ile Gly Cys Thr
      85                      90                      95

tta aat ttt cct att agt cct att gaa act gta cca gta aaa tta aaa      336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
      100                      105                      110

cca gga atg gat ggc cca aga gtt aaa caa tgg cca ttg aca gaa gaa      384
Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu
      115                      120                      125

aaa ata aaa gca tta gta gaa att tgt aca gaa ytg gaa gag gaa ggg      432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Xaa Glu Glu Glu Gly
      130                      135                      140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca ata ttt      480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe
      145                      150                      155                      160

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gcc ata aag aag aaa agt ggt aga tgg aga aaa ata gta gat ttt aga 528
 Ala Ile Lys Lys Lys Ser Gly Arg Trp Arg Lys Ile Val Asp Phe Arg
 165 170 175

gaa ctt aat aag aga act caa gat ttc tgg gaa gtt caa tta gga ata 576
 Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly Ile
 180 185 190

cca cat ccc gca ggg tta aaa aag aac aag tca gta aca att ctg gat 624
 Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Ile Leu Asp
 195 200 205

gtg ggt gat gca tat ttt tca gtt ccc tta gat aag gaa ttc agg aag 672
 Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Glu Phe Arg Lys
 210 215 220

tat act gca ttt acc ata cct agt ata aat aat gag aca cca ggg att 720
 Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly Ile
 225 230 235 240

aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca gca 768
 Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro Ala
 245 250 255

ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa caa 816
 Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys Gln
 260 265 270

aat cca gac ata gtt atc tat cag tac gtg gat gat ttg tat gta gga 864
 Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val Gly
 275 280 285

tct gat tta gaa ata ggg gag cat aga aca aaa ata gag gaa ctg aga 912
 Ser Asp Leu Glu Ile Gly Glu His Arg Thr Lys Ile Glu Glu Leu Arg
 290 295 300

car cat ctg tta arg tgg gga ttt ttc aca cca gaa caa aaa cat cag 960
 Gln His Leu Leu Xaa Trp Gly Phe Phe Thr Pro Glu Gln Lys His Gln
 305 310 315 320

aaa gaa cct ccm ttc cak tgg atg ggt tat gaa ctc cay cct gat aaa 1008
 Lys Glu Pro Xaa Phe Xaa Trp Met Gly Tyr Glu Leu His Pro Asp Lys
 325 330 335

tgg aca gta cas cct ata gtg ctg cca gaa aaa gat agc tgg act gtc 1056
 Trp Thr Val Xaa Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr Val
 340 345 350

aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag att 1104
 Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln Ile
 355 360 365

tac cca ggg
 Tyr Pro Gly 1113
 370

<210> 28
 <211> 1116
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)
 <220>

<221> CDS
 <222> (1)...(297)
 <223> HIV Protease

<221> CDS
 <222> (298)...(1116)
 <223> Portion of HIV Reverse Transcriptase

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<400> 28
cct caa atc act stt tgg caa cga ccc aty gtc tca ata aag ata ggg      48
Pro Gln Ile Thr Xaa Trp Gln Arg Pro Xaa Val Ser Ile Lys Ile Gly
  1                               5                               10                               15

ggg caa ata aag gaa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Ile Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
                               20                               25                               30

tta gaa gaa atg aat ttg cca gga aga tgg aag cca aaa atg ata gtg      144
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Val
                               35                               40                               45

gga att gga ggt ttt agc aaa gta aga caa tat gat cag ata ccc ata      192
Gly Ile Gly Gly Phe Ser Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile
  50                               55                               60

gaa atc tgc gga cgt aaa gtt gta ggt tca gta tta ata gga cct aca      240
Glu Ile Cys Gly Arg Lys Val Val Gly Ser Val Leu Ile Gly Pro Thr
  65                               70                               75                               80

cct gcc aac ata att gga aga aat ctg ttg act cag ctt ggc tgt act      288
Pro Ala Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr
                               85                               90                               95

tta aat ttt ccc att agt cct atk gaa act gta cca gta aaa tta aag      336
Leu Asn Phe Ile Ile Ser Pro Xaa Glu Thr Val Pro Val Lys Leu Lys
  100                              105                              110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca aaa gag      384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Lys Glu
  115                              120                              125

aaa ata aaa gca tta ata gaa att tgt aca gaa ttg gaa gaa gma gga      432
Lys Ile Lys Ala Leu Ile Glu Ile Cys Thr Glu Leu Glu Glu Xaa Gly
  130                              135                              140

aaa att aca aaa att ggg cct gaa aat ccg tac aat act cca ata ttt      480
Lys Ile Thr Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe
  145                              150                              155                              160

gcc ata aag aaa aar aac agt act aaa tgg aga aaa tta gta gac ttc      528
Ala Ile Lys Lys Lys Asn Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
                               165                               170                               175

agg gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga      576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
                               180                               185                               190

ata cca cat cct gca ggg tta aaa aag aaa aaa tca gta aca gta ctg      624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu
  195                               200                               205

gat gtg ggt gat gca tat ttt tca att ccc tta gat aaa gac ttc agg      672
Asp Val Gly Asp Ala Tyr Phe Ser Ile Pro Leu Asp Lys Asp Phe Arg
  210                               215                               220

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aar tat act gca ttt acc ata cct agt acg aat aat gag aca cca ggg      720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly
225                               230                               235                               240

att aga tat cag tat aat gtg ctt cca cag gga tgg aaa gga tca cca      768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
                               245                               250                               255

gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa      816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys
                               260                               265                               270

caa aat cca gac ata gtt atc tat caa tac gtg gat gat ttg ctt gta      864
Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Leu Val
                               275                               280                               285

gga tct gac tta gaa ata gag cag cat aga aca aaa ata gag gag cta      912
Gly Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Glu Glu Leu
                               290                               295                               300

aga caa cat ctg tgg aag tgg gga ttt tac aca cca gac aaa aaa cat      960
Arg Gln His Leu Trp Lys Trp Gly Phe Tyr Thr Pro Asp Lys Lys His
305                               310                               315                               320

cag aaa gaa ccc cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat     1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
                               325                               330                               335

aaa tgg aca gka cag cct ata gtg ctg cca gaa aaa gac agc tgg act     1056
Lys Trp Thr Xaa Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
                               340                               345                               350

gtc aat gac ata caa aag tta gtg gga aaa tta aat tgg gca agt cag     1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
                               355                               360                               365

att tat cca ggg
Ile Tyr Pro Gly
370

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<210> 29
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

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<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

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<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

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<400> 29
cct cag atc act ctt tgg caa cga ccc atc gtc aca ata aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Ile Gly
1                               5                               10                               15

ggg caa cta aag gaa gct cta ata gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Ile Asp Thr Gly Ala Asp Asp Thr Val
                               20                               25                               30

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tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa ata ata ggg Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Ile Ile Gly 35 40 45	144
gga att gga ggt ctt gtc aaa gta aga cag tat gat cag ata ccc ata Gly Ile Gly Gly Leu Val Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile 50 55 60	192
gaa atc tgt gga cat aaa gtt ata ggt aca gtw tta gta gga cct aca Glu Ile Cys Gly His Lys Val Ile Gly Thr Xaa Leu Val Gly Pro Thr 65 70 75 80	240
cct gcc aac ata att gga aga aat ctg ttg act cag ctt ggt tgc act Pro Ala Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr 85 90 95	288
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca ggg atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gag aag gag gga Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly 130 135 140	432
aag att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gcc ata aag aaa aag aac agt act agg tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asn Ser Thr Arg Trp Arg Lys Leu Val Asp Phe 165 170 175	528
aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat ccc gca ggg tta aaa aag aac aaa tca gca aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Ala Thr Val Leu 195 200 205	624
gat gtg ggc gat gca tat ttt tca gtt ccc tta gac aaa gaa ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Glu Phe Arg 210 215 220	672
aag tat act gca ttt acy ata cct agt ata aac aat gaa aca cca ggg Lys Tyr Thr Ala Phe Xaa Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240	720
tar ata tca gtg tac aat gtr ctt cca caa gga tgg aaa gga tca cma Xaa Ile Ser Val Tyr Asn Xaa Leu Pro Gln Gly Trp Lys Gly Ser Xaa 245 250 255	768
gca ata ttc maa agt agc atg aca aga atc tta gag cct ttt aga aaa Ala Ile Phe Xaa Ser Ser Met Thr Arg Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gaa ata gtt atc tat caa tac gtg gat gat ttg tat gta Gln Asn Pro Glu Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val 275 280 285	864

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gga tct gac tta gaa ata ggg cag cat aga aca aaa gta gag gaa ctg      912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Val Glu Glu Leu
290                               295                               300

aga caa cat ctg ttg agg tgg gga ttt ttc aca cca gac caa aaa cat      960
Arg Gln His Leu Leu Arg Trp Gly Phe Phe Thr Pro Asp Gln Lys His
305                               310                               315                               320

cag aaa gaa ccc cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat      1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
                               325                               330                               335

aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act      1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
                               340                               345                               350

gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt cag      1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
                               355                               360                               365

att tac gcn ggg
Ile Tyr Ala Gly
370

<210> 30
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

<400> 30
cct caa atc act ctt tgg caa cga ccc cty gtc aca ata aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Xaa Val Thr Ile Lys Ile Gly
1                               5                               10                               15

ggg caa cta aag gaa gct yta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Xaa Leu Asp Thr Gly Ala Asp Asp Thr Val
                               20                               25                               30

tta gaa gaa atg agc tta cca gga aga tgg aaa cca aaa atg ata ggg      144
Leu Glu Glu Met Ser Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
35                               40                               45

gga att gga ggk ttt atc aaa gtg agm cag tat gat cag ata ctc ata      192
Gly Ile Gly Xaa Phe Ile Lys Val Xaa Gln Tyr Asp Gln Ile Leu Ile
50                               55                               60

gaa aty tgt gga cat aaa gct ata ggt aca gtr tta ata gga cct aca      240
Glu Xaa Cys Gly His Lys Ala Ile Gly Thr Xaa Leu Ile Gly Pro Thr
65                               70                               75                               80

cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act      288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
                               85                               90                               95

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tta aat ttt ccc att agt cct att gaa act gta cca gta aaa ttg aaa Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtc aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa ggr Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Xaa 130 135 140	432
aaa att aca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Thr Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gcc ata aag aag aaa aac agt gat aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asn Ser Asp Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528
aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat cca gca ggg tta aaa cag aaa aag tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Gln Lys Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttt tca gta ccc tta gat gaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg 210 215 220	672
aag tat act gca ttt acc ata cct agt gta aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Val Asn Asn Glu Thr Pro Gly 225 230 235 240	720
gtt aga tat cag tac aat gta ctc cca cag gga tgg aaa gga tca cca Val Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttt caa agt agc atg aca aaa atc tta gag cct ttt agg aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gaa ata gtt atc tat caa tac gtg gat gat ttg tat gta Gln Asn Pro Glu Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac tta gaa ata ggg cag cat aga gca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Leu 290 295 300	912
aga caa cat ctg ttg agg tgg gga ttc tac aca cca gac aaa aaa cat Arg Gln His Leu Leu Arg Trp Gly Phe Tyr Thr Pro Asp Lys Lys His 305 310 315 320	960
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056

gtc aat gac ata cag aag tta gta ggg aaa tta aat tgg gca agt cag 1104
 Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
 355 360 365

att tat gca gga 1116
 Ile Tyr Ala Gly
 370

<210> 31
 <211> 1117
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)

<220>
 <221> CDS
 <222> (1)...(297)
 <223> HIV Protease

<221> CDS
 <222> (298)...(1116)
 <223> Portion of HIV Reverse Transcriptase

<400> 31
 cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata aag ata ggg 48
 Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly
 1 5 10 15

ggg caa tta aag gaa gct cta tta gat aca gga gca gat gat aca gta 96
 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
 20 25 30

cta gaa gac gtg cat ttg cca gga aaa tgg aaa cca aaa atg ata ggg 144
 Leu Glu Asp Val His Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly
 35 40 45

gga att gga ggt ttt atc aaa gta aga cag tat gat gag gta ccc ata 192
 Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Glu Val Pro Ile
 50 55 60

gaa ctc tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca 240
 Glu Leu Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr
 65 70 75 80

ccc gtc aac ata att gga aga aat ctg wtg act caa ctt ggg tgc act 288
 Pro Val Asn Ile Ile Gly Arg Asn Leu Xaa Thr Gln Leu Gly Cys Thr
 85 90 95

cta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
 100 105 110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
 115 120 125

aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa ggg 432
 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
 130 135 140

aaa att tca aga gtt ggg cct gaa aat cca tac aat act cca gta ttt 480
 Lys Ile Ser Arg Val Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
 145 150 155 160

gyc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc Xaa Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528
aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cay ccc gca ggg tta aaa aag aaa aaa tca gta aca gta ctr Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Xaa 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gaa ttc aga Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Glu Phe Arg 210 215 220	672
aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240	720
att aga tac cag tac aat gtg ctt cca caa gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agt agc atg aca aaa atc tta gat cct ttt agg aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Asp Pro Phe Arg Lys 260 265 270	816
caa aac cca gac ata gtt atc tat caa tac gtg gat gat ttg tat gta Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val 275 280 285	864
gga tcy gac tta gaa ata gga cag cat agr rca aaa ata gaa gaa ctg Gly Xaa Asp Leu Glu Ile Gln His Xaa Xaa Lys Ile Glu Glu Leu 290 295 300	912
aga caa cat ctg ttg aag tgg gga ttt acc aca cca gac aag aaa cat Arg Gln His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His 305 310 315 320	960
car aaa gaa cct cca ttt ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gtg cag cct ata gtg ctg cca gaa aag gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056
gtc aat gac ant aca gaa gtt agt ggg aaa att gaa ttg ggc aag tca Val Asn Asp Xaa Thr Glu Val Ser Gly Lys Ile Glu Leu Gly Lys Ser 355 360 365	1104
gat tta tgc agg g Asp Leu Cys Arg 370	1117

<210> 32
 <211> 1116
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)
 <220>

<221> CDS
 <222> (1)...(297)
 <223> HIV Protease

<221> CDS
 <222> (298)...(1116)
 <223> Portion of HIV Reverse Transcriptase

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<400> 32
cct caa atc act ctt tgg caa cga ccc cty gtc gca ata agg ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Xaa Val Ala Ile Arg Ile Gly
1          5          10          15

ggg caa cta aag gaa gcc cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
          20          25          30

tta gaa gac atg gag ttg cca gga aga tgg aag cca aaa atg ata ggg      144
Leu Glu Asp Met Glu Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
          35          40          45

gga att gga ggt ttt atc aaa gta aam cag tat gat cag ata ctt gta      192
Gly Ile Gly Gly Phe Ile Lys Val Xaa Gln Tyr Asp Gln Ile Leu Val
          50          55          60

gaa atc tgt gga cat aaa gct gta ggt aca gta tta ata gga cct aca      240
Glu Ile Cys Gly His Lys Ala Val Gly Thr Val Leu Ile Gly Pro Thr
65          70          75          80

cct gtc aac ata att gga aga aat ttg ttg act cag att ggc tgc act      288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
          85          90          95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag      336
Leu Asn Phe Phe Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
          100          105          110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gag      384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
          115          120          125

aaa ata aaa gca tta gta gaa atc tgt aca gaa ttg gaa aag gaa gga      432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly
          130          135          140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt      480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
145          150          155          160

gct ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc      528
Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
          165          170          175

aga gaa ctt aat aaa aga act caa gac ttt tgg gaa gtt caa tta gga      576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
          180          185          190

ata cca cat ccc gca ggg tta aaa aag aaa aaa tcc gtg aca gta ctg      624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu
          195          200          205

gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttt aga      672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg
210          215          220

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aag tat act gca ttt acc aya cct sgt ata aac aat gag aca cca ggg 720
Lys Tyr Thr Ala Phe Thr Xaa Pro Xaa Ile Asn Asn Glu Thr Pro Gly
225 230 235 240

att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tcc cca 768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
245 250 255

gca ata ttt caa agc agc atg aca aaa atc tta gag cct ttt aga aaa 816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys
260 265 270

caa aat cca gac wta gtt wtc tat caa twc ata gat gat ctg tat gta 864
Gln Asn Pro Asp Xaa Val Xaa Tyr Gln Xaa Ile Asp Asp Leu Tyr Val
275 280 285

ggc tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg 912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu
290 295 300

aga cag cat ctg tgg aag tgg ggg ttt tac aca cca gac aaa aaa cat 960
Arg Gln His Leu Trp Lys Trp Gly Phe Tyr Thr Pro Asp Lys Lys His
305 310 315 320

cag aaa gaa cct cca ttt ctt tgg atg ggt tat gaa ctc cat cct gat 1008
Gln Lys Glu Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
325 330 335

aaa tgg aca gta cag cct ata atg ctg cca gaa aaa gac agc tgg act 1056
Lys Trp Thr Val Gln Pro Ile Met Leu Pro Glu Lys Asp Ser Trp Thr
340 345 350

gtc aat gac ata cag aar tta gtg gga aaa ttg aat tgg gca agt cag 1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
355 360 365

att tac cca ggg 1116
Ile Tyr Pro Gly
370

<210> 33
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

<400> 33
cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata aag ata ggg 48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly
1 5 10 15

ggg caa cta aag gaa gct cta tta kat aca gga gca gat gat aca gtm 96
Gly Gln Leu Lys Glu Ala Leu Leu Xaa Thr Gly Ala Asp Asp Thr Xaa
20 25 30

tta gaa gac atg act ttg cca gga aga tgg aaa cca aaa atg ata ggg Leu Glu Asp Met Thr Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly 35 40 45	144
gga att gga ggt ttt atc aaa gta aaa cag tat gag gag ata ccc ata Gly Ile Gly Gly Phe Ile Lys Val Lys Gln Tyr Glu Glu Ile Pro Ile 50 55 60	192
gaa atc tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr 65 70 75 80	240
cct gtc aac ata att gga aga aat ttg ttg act cag att ggt tgc act Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr 85 90 95	288
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aaa Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca ttw gta gaa att tgt gca gaa ctg gaa aag gaa ggg Lys Ile Lys Ala Xaa Val Glu Ile Cys Ala Glu Leu Glu Lys Glu Gly 130 135 140	432
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gcc ata aag aaa aaa gac ggt act aaa tgg aga aag gta aca gat ttt Ala Ile Lys Lys Lys Asp Gly Thr Lys Trp Arg Lys Val Thr Asp Phe 165 170 175	528
aga gaa ctt aat aag agg ach caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Xaa Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat ccc tca ggg tta aaa aag aaa aaa tca gta aca gta ctg Ile Pro His Pro Ser Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg 210 215 220	672
aag tat act gca ttt acc ata cct agt ata aac aat gcg aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Ala Thr Pro Gly 225 230 235 240	720
att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gac atg gtt atc tat caa tac atg gat gat ttg tat gta Gln Asn Pro Asp Met Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864

gga tct gat tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg 912
 Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu
 290 295 300

aga caa cat ctg ttg aag tgg ggt ttt acc aca cca gac aaa aaa cat 960
 Arg Gln His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His
 305 310 315 320

cag aaa gaa cct cca ttt ctt tgg atg ggt tat gaa ctc cat cct gat 1008
 Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
 325 330 335

aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act 1056
 Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
 340 345 350

gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag 1104
 Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
 355 360 365

att tat tca ggg 1116
 Ile Tyr Ser Gly
 370

<210> 34
 <211> 1119
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)

<220>
 <221> CDS
 <222> (1)...(297)
 <223> HIV Protease

<221> CDS
 <222> (298)...(1119)
 <223> Portion of HIV Reverse Transcriptase

<400> 34
 cct cag atc act ctt tgg caa cga ccc atc gtc aca ata aag ata ggg 48
 Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Ile Gly
 1 5 10 15

ggg cag cta aag gaa gct cta ttr gac aca gga gca gat gat aca gta 96
 Gly Gln Leu Lys Glu Ala Leu Xaa Asp Thr Gly Ala Asp Asp Thr Val
 20 25 30

tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa ata ata ggg 144
 Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Ile Ile Gly
 35 40 45

gga att gga ggt ttt att aaa gta aaa cag tat gaa cag ata acc ata 192
 Gly Ile Gly Gly Phe Ile Lys Val Lys Gln Tyr Glu Gln Ile Thr Ile
 50 55 60

gam atc tgt gga cat aaa gct aca ggt aca gta tta gta gga cct aca 240
 Xaa Ile Cys Gly His Lys Ala Thr Gly Thr Val Leu Val Gly Pro Thr
 65 70 75 80

cct gtc aac gta att gga aga aat atg atg act cag att ggt tgc act 288
 Pro Val Asn Val Ile Gly Arg Asn Met Met Thr Gln Ile Gly Cys Thr
 85 90 95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aga gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta gta gaa att tgt aca gaa ttg gaa aag gaa ggg Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly 130 135 140	432
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528
aga gaa ctt aac aag aga act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat ccc gca ggg tta cca aag aac aaa tca gta acg gta ctg Ile Pro His Pro Ala Gly Leu Pro Lys Asn Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtt cct tta gat gaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg 210 215 220	672
aag tac act gca ttt acc ata cct agg tat aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Ile Pro Arg Tyr Asn Asn Glu Thr Pro Gly 225 230 235 240	720
act aga tat cag tac aat gtg ctt cct atg gga tgg aaa gga tca cca Thr Arg Tyr Gln Tyr Asn Val Leu Pro Met Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aga Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Arg 260 265 270	816
caa aat cca gac ata gtt atc tat caa tac gtg gat gac ttg tat gta Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac tta gag ata ggg cag cat aga gcg aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Leu 290 295 300	912
aga gaa cat ctg tgg aag tgg ggt ttt tac aca cca gac aaa aaa cat Arg Glu His Leu Trp Lys Trp Gly Phe Tyr Thr Pro Asp Lys Lys His 305 310 315 320	960
cag aaa gaa cct cca ttc cat tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe His Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta cag cct ata gtg ctg cca gaa aag gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056

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gtc aat gac ata cag aaa tta gtg ggr aaa att gaa ttt ggg cga gtc      1104
Val Asn Asp Ile Gln Lys Leu Val Xaa Lys Ile Glu Phe Gly Arg Val
      355                      360                      365

aga ttt amc caa ggg
Arg Phe Xaa Gln Gly
      370

<210> 35
<211> 1115
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1115)
<223> Portion of HIV Reverse Transcriptase

<400> 35
cct cag atc act ctt tgg caa cga ccc cty gtc cca ata arg ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Xaa Val Pro Ile Xaa Ile Gly
      1                      5                      10                      15

ggg caa tta aag gaa gct cta cta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
      20                      25                      30

tta gaa gac atg aat tta cca gga aga tgg aaa cca aaa atg ata ggg      144
Leu Glu Asp Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
      35                      40                      45

gga att gga ggt ttt atc aar gta aaa cag tat gat cag ata ccc ata      192
Gly Ile Gly Gly Phe Ile Lys Val Lys Gln Tyr Asp Gln Ile Pro Ile
      50                      55                      60

gaa atc tgt ggg cat aaa gct ata ggt aca gta tta gta gga cct aca      240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr
      65                      70                      75                      80

cct gtc aac ata att gga aga aat ctg ttg act cag ctt ggt tgc act      288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr
      85                      90                      95

cta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag      336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
      100                      105                      110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa      384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
      115                      120                      125

aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa gga      432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
      130                      135                      140

aaa att tca aaa att gga cct gaa aat cca tac aat act cca gta ttt      480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
      145                      150                      155                      160

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gcc ata aag aaa aag gac agt act aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528
aga gaa ctt aat aag aga act caa gac ttt tgg gaa gtc caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta tta Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg gga gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg 210 215 220	672
aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240	720
att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aag Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gac ata gtc ata tat caa tac atg gat gat ttg tat gta Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864
ggg tct gac tta gaa ata gga cag cat aga aca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300	912
aga caa cac ttg ttg maa tgg gga ttc acc aca cca gac aaa aag cat Arg Gln His Leu Leu Xaa Trp Gly Phe Thr Thr Pro Asp Lys Lys His 305 310 315 320	960
cag aaa gaa ccc cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta cag cct ata kaa ctg cca gaa aaa gac agc tgg ctg Lys Trp Thr Val Gln Pro Ile Xaa Leu Pro Glu Lys Asp Ser Trp Leu 340 345 350	1056
tca atg aca tac aga aat tag tgg gaa agt tga att ggg caa gtc aaa Ser Met Thr Tyr Arg Asn * Trp Glu Ser * Ile Gly Gln Val Lys 355 360 365	1104
ttt atg cng gg Phe Met Xaa	1115

<210> 36

<211> 1116

<212> DNA

<213> Human Immunodeficiency Virus (HIV)

<220>

<221> CDS
 <222> (1)...(297)
 <223> HIV Protease

<221> CDS
 <222> (298)...(1116)
 <223> Portion of HIV Reverse Transcriptase

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<400> 36
cct cag atc act ctt tgg caa cga cca gtc gtc aca ata aag gta ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Val Val Thr Ile Lys Val Gly
1          5          10

ggg cag cta aag gaa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
          20          25          30

tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atg ata ggg      144
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
          35          40          45

gga att gga ggt ttt rtc aaa gta aga cag tat gat caa ata ccc ata      192
Gly Ile Gly Gly Phe Xaa Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile
          50          55          60

gaa atc tgt gga cat aaa gct aca ggt aca gta tta gta gga cct aca      240
Glu Ile Cys Gly His Lys Ala Thr Gly Thr Val Leu Val Gly Pro Thr
65          70          75          80

cct gyc aac ata att gga aga aat ctg ttg act cag att ggg tgc act      288
Pro Xaa Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
          85          90          95

tta aat ttt cct att agt cct att gaa act gta cca gta aaa tta aag      336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
          100          105          110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ctg aca gaa gaa      384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
          115          120          125

aaa ata aaa gca tta gta gaa att tgt gca gaa ttg gaa aag gaa ggg      432
Lys Ile Lys Lys Ala Leu Val Glu Ile Cys Ala Glu Leu Glu Lys Glu Gly
130          135          140

aag att tca aaa att ggg ccy gaa aat cca tac aay act cca gta ttt      480
Lys Ile Ser Lys Ile Gly Xaa Glu Asn Pro Tyr Asn Thr Pro Val Phe
145          150          155          160

gcc ata aag aaa aar aac agt act ara tgg aga aaa kta gta gat ttc      528
Ala Ile Lys Lys Lys Asn Ser Thr Xaa Trp Arg Lys Xaa Val Asp Phe
          165          170          175

aga gaa ctt aat aag aga act caa gat ttc tgg gaa gtt caa tta gga      576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
          180          185          190

ata cca cat ccc gca ggg cta aag aag aaa aaa tca gta aca gta ctg      624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu
          195          200          205

gat gtg ggt gat gca tat ttt tca gtt ccc ttg gat gaa gac ttc aga      672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg
210          215          220

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aag tat aca gcc ttt acc tat act ggt tcc aac aat gag aca cca ggg      720
Lys Tyr Thr Ala Phe Thr Tyr Thr Gly Ser Asn Asn Glu Thr Pro Gly
225                      230                      235                      240

att aga tat car tac aat gtg ctt cca cag gga tgg aaa gga tca cca      768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
                      245                      250                      255

gca ata ttc caa agc agc atg aca aaa gtc tta gaa cct ttt aga aaa      816
Ala Ile Phe Gln Ser Ser Met Thr Lys Val Leu Glu Pro Phe Arg Lys
                      260                      265                      270

caa aat cca gac ata gtt atc tgt caa tac atg gat gat ttg tat gta      864
Gln Asn Pro Asp Ile Val Ile Cys Gln Tyr Met Asp Asp Leu Tyr Val
                      275                      280                      285

gga tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg      912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu
                      290                      295                      300

aga caa cat ctg tta agg tgg gga ttt tac aca cca gac gaa aaa cat      960
Arg Gln His Leu Leu Arg Trp Gly Phe Tyr Thr Pro Asp Glu Lys His
305                      310                      315                      320

cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gac      1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
                      325                      330                      335

aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act      1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
                      340                      345                      350

gtt aat gac ata cag aaa tta gtg gga aaa ttg aat tgg gcc agt cag      1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
                      355                      360                      365

att tac cca ggg
Ile Tyr Pro Gly
370

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<210> 37
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

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<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

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<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

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<400> 37
cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata aaa ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly
1                      5                      10                      15

ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
                      20                      25                      30

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tta gaa gac atg aat ttg cca gga aga tgg aaa cca aaa atg ata ggg Leu Glu Asp Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly 35 40 45	144
gga att gga ggt ttt atc aaa gta aga cag tat gat cag gta ccc ata Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Val Pro Ile 50 55 60	192
gaa atc tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr 65 70 75 80	240
cct gtc aac ata att gga aga aat ctg atg aca cag ctt ggt tgt act Pro Val Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Leu Gly Cys Thr 85 90 95	288
tta aat ttt cct att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa ggg Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly 130 135 140	432
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528
agg gaa ctt aat aag aaa act caa gac ttc tgg gaa gtt caa tta ggg Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat cct gca gga tta aaa aag aat aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg 210 215 220	672
aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240	720
att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agt agc atg aca aaa att tta gat cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Asp Pro Phe Arg Lys 260 265 270	816
cag aat cca gat ata gtt atc tat caa tac atg gat gat ttg tat gta Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864

gga tct gac tta gag ata ggg cag cat aga gca aaa ata gag gaa ctg 912
 Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Leu
 290 295 300
 aga gca cat ctg ttg aag tgg gga ttt acc acc cca gac aaa aaa cat 960
 Arg Ala His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His
 305 310 315 320
 cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat 1008
 Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
 325 330 335
 aaa tgg aca gta cag cct ata gtg ctg cca gaa aag gac agc tgg act 1056
 Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
 340 345 350
 gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt cag 1104
 Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
 355 360 365
 att tac gca ggg 1116
 Ile Tyr Ala Gly
 370

<210> 38
 <211> 1117
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)

<220>
 <221> CDS
 <222> (1)...(297)
 <223> HIV Protease
 <221> CDS
 <222> (298)...(1117)
 <223> Portion of HIV Reverse Transcriptase

<400> 38
 cct caa tca ctt ctt tgg caa cga ccc mtc gtc aca ata aag gta ggg 48
 Pro Gln Ser Leu Leu Trp Gln Arg Pro Xaa Val Thr Ile Lys Val Gly
 1 5 10 15
 ggg cag cta aag gaa gct cta tta gat aca gga gca gat gat aca ata 96
 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Ile
 20 25 30
 tta gaa gac aya rat ttg cca ggg aga tgg aaa cca aaa ata ata ggg 144
 Leu Glu Asp Xaa Xaa Leu Pro Gly Arg Trp Lys Pro Lys Ile Ile Gly
 35 40 45
 gga att gga ggt ttt atc aga gta aga cag tat gat cag gta ccc ata 192
 Gly Ile Gly Gly Phe Ile Arg Val Arg Gln Tyr Asp Gln Val Pro Ile
 50 55 60
 gaa atc tgt gga cat aaa gtt gta agt aca gta tta gta gga cct aca 240
 Glu Ile Cys Gly His Lys Val Val Ser Thr Val Leu Val Gly Pro Thr
 65 70 75 80
 cct gcc aac ata att gga aga aat ctg atg act cag att ggt tgc act 288
 Pro Ala Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Ile Gly Cys Thr
 85 90 95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag	336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys	
100 105 110	
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa	384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu	
115 120 125	
aaa ata aaa gca tta gta gaa att tgt gaa gaa ttg gaa aag gat ggg	432
Lys Ile Lys Ala Leu Val Glu Ile Cys Glu Glu Leu Glu Lys Asp Gly	
130 135 140	
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt	480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe	
145 150 155 160	
gcc ata aag aaa aag aac agt act aaa tgg aga aaa tta gta gat ttc	528
Ala Ile Lys Lys Lys Asn Ser Thr Lys Trp Arg Lys Leu Val Asp Phe	
165 170 175	
aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga	576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly	
180 185 190	
ata cca cat cct gca gga tta aaa aag aaa aaa tca gta aca gta ctg	624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu	
195 200 205	
gat gtg ggt gat gca tat ttt tca att ccc tta gat gaa gac ttc aga	672
Asp Val Gly Asp Ala Tyr Phe Ser Ile Pro Leu Asp Glu Asp Phe Arg	
210 215 220	
aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg	720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly	
225 230 235 240	
att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca	768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro	
245 250 255	
tca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa	816
Ser Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys	
260 265 270	
caa aat cca gac ata gtc atc tat caa tat atg gat gat ttg tat gta	864
Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val	
275 280 285	
gga tct gac tta gag ata ggg cag cat aga aca aaa ata gag gaa ctg	912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu	
290 295 300	
aga cag cat ctg tgg aag tgg ggg ttt tac aca cca gac ara aaa cat	960
Arg Gln His Leu Trp Lys Trp Gly Phe Tyr Thr Pro Asp Xaa Lys His	
305 310 315 320	
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gac	1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp	
325 330 335	
aaa tgg aca gta cag cct ata gtg ctg cca gaa aag gac agc tgg act	1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr	
340 345 350	

gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag 1104
 Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
 355 360 365

att tan tsc agg g 1117
 Ile Xaa Xaa Arg
 370

<210> 39
 <211> 1128
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)

<220>
 <221> CDS
 <222> (1)...(297)
 <223> HIV Protease

<221> CDS
 <222> (298)...(1128)
 <223> Portion of HIV Reverse Transcriptase

<400> 39
 cct cag atc act ctt tgg caa cga cca ttc gtc aca ata aaa ata ggg 48
 Pro Gln Ile Thr Leu Trp Gln Arg Pro Phe Val Thr Ile Lys Ile Gly
 1 5 10 15

ggg caa cta aag gaa gct ata tta gac aca gga gca gat gat aca gta 96
 Gly Gln Leu Lys Glu Ala Ile Leu Asp Thr Gly Ala Asp Thr Val
 20 25 30

tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atg ata ggg 144
 Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
 35 40 45

gga att gga ggt ttt mtc aaa gta aga cag tat gat cag gta ccc ata 192
 Gly Ile Gly Gly Phe Xaa Lys Val Arg Gln Tyr Asp Gln Val Pro Ile
 50 55 60

gaa atc tgt gga cat aaa gtt atg agt aca gta tta ata gga cct aca 240
 Glu Ile Cys Gly His Lys Val Met Ser Thr Val Leu Ile Gly Pro Thr
 65 70 75 80

cct gtc aac ata att gga aga aat ctg atg act cag mtt ggc tgc act 288
 Pro Val Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Xaa Gly Cys Thr
 85 90 95

tta aat ttt ccc att agt cct att gaa act gwa cca gta aaa tta aag 336
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Xaa Pro Val Lys Leu Lys
 100 105 110

cca ggg atg gac ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
 115 120 125

aaa ata aaa gca tta gta gaa att tgt aca gaa ttg gaa aag gaa gga 432
 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly
 130 135 140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt 480
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
 145 150 155 160

gcc ata aag aaa aaa gac agt aat aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asp Ser Asn Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528
aga gaa ctt aat aag aga act caa gat ttc tgg gaa gtc caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat cct gca ggg tta aaa aag aac aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat raa gat tca gra Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Xaa Asp Ser Xaa 210 215 220	672
agt aca ctg cat tta cca tac cta gta cgr acc aat gag aca cca ggg Ser Thr Leu His Leu Pro Tyr Leu Val Xaa Thr Asn Glu Thr Pro Gly 225 230 235 240	720
att aga tat caa tac aat gtg ctt cca caa gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gac tta gtt atc tgt caa tac atg gat gat ttg tat gta Gln Asn Pro Asp Leu Val Ile Cys Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864
gga tct gat tta gaa ata gag cag cat aga aca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300	912
aga caa cat ctg tgg aag tgg ggg ttt tac aca cca gac aaa aaa cat Arg Gln His Leu Trp Lys Trp Gly Phe Tyr Thr Pro Asp Lys Lys His 305 310 315 320	960
cag aaa gaa cct cca ttc cgt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Arg Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta caa gcc tat aaa gct gcc aga aaa aga cag ctg gac Lys Trp Thr Val Gln Ala Tyr Lys Ala Ala Arg Lys Arg Gln Leu Asp 340 345 350	1056
tgt caa tga cat tac mag aaa gtt agt ggg gaa aat tgg aat ttg ggg Cys Gln * His Tyr Xaa Lys Val Ser Gly Glu Asn Trp Asn Leu Gly 355 360 365	1104
caa ggt cag att tat tgc cag ggg Gln Gly Gln Ile Tyr Cys Gln Gly 370 375	1128

<210> 40
 <211> 1120
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)

<220>

<221> CDS
 <222> (1)...(297)
 <223> HIV Protease

<221> CDS
 <222> (298)...(1120)
 <223> Portion of HIV Reverse Transcriptase

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<400> 40
cct cag atc act ctt tgg caa cga ccc ctc gtt gca ata aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Ala Ile Lys Ile Gly
  1                      5                      10                      15

gga cag cta aag gaa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
                      20                      25                      30

tta gaa gaa atg agt ttg cca gga aga tgg aaa cca aaa atg ata ggg      144
Leu Glu Glu Met Ser Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
                      35                      40                      45

gga att gga ggt ttt atc aaa gta aga car tat gat cag ata ccm rta      192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Xaa Xaa
                      50                      55                      60

gaa att tgc gga cat aaa gct gta ggt aca gta tta gta gga cct aca      240
Glu Ile Cys Gly His Lys Ala Val Gly Thr Val Leu Val Gly Pro Thr
                      65                      70                      75                      80

cct gtc aac ata att gga aga aat ctg ttg act cag mtt ggt tgc act      288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Xaa Gly Cys Thr
                      85                      90                      95

tta aat ttt ccc att agt cct att gaa act gta cca gtg aaa tta aag      336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
                      100                      105                      110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa      384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
                      115                      120                      125

aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa ggg      432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
                      130                      135                      140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt      480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
                      145                      150                      155                      160

gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc      528
Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
                      165                      170                      175

aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga      576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
                      180                      185                      190

ata cca cat cct gca ggg tta aaa aag aaa aaa tca gta aca gta ctg      624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu
                      195                      200                      205

gat gtg ggt gat gca tat ttt tca gtt cct tta gat gaa gac ttc agr      672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Xaa
                      210                      215                      220

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aag tat act gca ttt acc ata cct agt aca aac aat gag aca cca ggg 720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly
225 230 235 240

att aga tat cag tcc aat gtg ctt cca cag gga tgg aaa gga tca cca 768
Ile Arg Tyr Gln Ser Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
245 250 255

gca ata ttc caa agt agc atg aca aaa atc cta gaa cct ttt agg aaa 816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys
260 265 270

caa aat cca gat ata gtt atc tat caa tac atg gat gat cta tat gta 864
Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val
275 280 285

gga tct gac tta gaa ata gaa cag cat aga aca aaa ata gag gaa ctg 912
Gly Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Glu Glu Leu
290 295 300

aga caa cat ctg ttg agg tgg ggg ttt acc acc cca gac aaa aaa cat 960
Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His
305 310 315 320

cag aaa gaa ccc cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat 1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
325 330 335

aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act 1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
340 345 350

gtc aat gac nat aca aaa gtt agt ggg gaa aat tga att ggg sca agt 1104
Val Asn Asp Xaa Thr Lys Val Ser Gly Glu Asn * Ile Gly Xaa Ser
355 360 365

cag att tat tgg agg g 1120
Gln Ile Tyr Trp Arg
370

<210> 41
<211> 1059
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1059)
<223> Portion of HIV Reverse Transcriptase

<400> 41
cct caa atc act ctt tgg cag cga ccc gtt gtc aca ata aac ata ggg 48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Val Val Thr Ile Asn Ile Gly
1 5 10 15

ggg caa cta aag gaa gct cta tta gac aca gga gca gat gat aca gta 96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
20 25 30

tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atg ata ggg Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly 35 40 45	144
gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ccc ata Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile 50 55 60	192
gaa atc tgt gga cat aaa act ata ggt aca gta tta ata gga cct aca Glu Ile Cys Gly His Lys Thr Ile Gly Thr Val Leu Ile Gly Pro Thr 65 70 75 80	240
cct gtc aac ata att gga aga aat ctg ttg act cag att ggc tgc act Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr 85 90 95	288
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta ata gaa att tgt aca gaa atg gaa aag gaa ggg Lys Ile Lys Ala Leu Ile Glu Ile Cys Thr Glu Met Glu Lys Glu Gly 130 135 140	432
aaa att tca aaa att ggg cct gaa aac ccg tac aat act cca gtc ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gcc ata aag aaa aaa gat agt act aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528
aga gaa ctt aac aag aaa act caa gac ttc tgg gaa att caa tta gga Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Ile Gln Leu Gly 180 185 190	576
ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttc tca gtt cct tta gat aaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg 210 215 220	672
aag tat act gca ttt acc ata cct agt aca aac aat gag acg cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly 225 230 235 240	720
att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gcc ata nnn nnn nnn nnn nnn nnn nnn nnn nnn nnn nnn nnn nnn Ala Ile Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa 260 265 270	816
nnn nnn nnn nnn nnn nnn nnn tat caa tac atg gat gat ttg tat gta Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864

gga tct gac tta gaa ata gag cag cat aga aca aaa ata gag aaa ctg 912
 Gly Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Glu Lys Leu
 290 295 300

aga caa cat ctg ttg agg tgg gga ttt acc aca cca gat aaa aaa cat 960
 Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His
 305 310 315 320

cag aaa gaa cct cca ttt ctt tgg atg ggt tat gaa ctc cat cct gat 1008
 Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
 325 330 335

aaa tgg aca gta cag cct ata gta ctg cca gaa aaa gac agc tgg act 1056
 Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
 340 345 350

gtc 1059
 Val

<210> 42
 <211> 1053
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)

<220>
 <221> CDS
 <222> (1)...(297)
 <223> HIV Protease

<221> CDS
 <222> (298)...(1053)
 <223> Portion of HIV Reverse Transcriptase

<400> 42
 cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata arg ata ggg 48
 Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Xaa Ile Gly
 1 5 10 15

ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta 96
 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
 20 25 30

tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atg ata ggg 144
 Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
 35 40 45

gga att gga ggt ttt atm aaa gta aga cag tat gat cag ata cyc ata 192
 Gly Ile Gly Gly Phe Xaa Lys Val Arg Gln Tyr Asp Gln Ile Xaa Ile
 50 55 60

gaa atc tgt gga yat aaa gct ata ggt acr gta tta gta gga ccc acg 240
 Glu Ile Cys Gly Xaa Lys Ala Ile Gly Xaa Val Leu Val Gly Pro Thr
 65 70 75 80

cct gtc aac rta att gga aga aat ctg wtg act cag att ggt tgc act 288
 Pro Val Asn Xaa Ile Gly Arg Asn Leu Xaa Thr Gln Ile Gly Cys Thr
 85 90 95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
 100 105 110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa gga Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly 130 135 140	432
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa ttr gta gat ttc Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Xaa Val Asp Phe 165 170 175	528
aga gaa ctt aat aag aaa act caa gac ttc tgg gaa gtc caa tta gga Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat ccc gca ggg tta aag aag aaa aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg 210 215 220	672
aag tat act gca ttt acc ata cct agt gta aac aat gag aca cca kgg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Val Asn Asn Glu Thr Pro Xaa 225 230 235 240	720
att aga tay cag tac aat gtg ctt cca caa gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata tty caa tgt agc atg aca aaa atc tta gag cct ttt aga aag Ala Ile Phe Gln Cys Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gac cta gtt att tat caa tac atg gat gat ttg tat gta Gln Asn Pro Asp Leu Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300	912
aga caa cat ctg ttg ara tgg gga ttt acc aca cca gac aaa aaa cat Arg Gln His Leu Leu Xaa Trp Gly Phe Thr Thr Pro Asp Lys Lys His 305 310 315 320	960
cag aaa gaa ccc cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg gca gtg caa cct ata gtg ctg cca gaa aaa gac agc tgg Lys Trp Ala Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp 340 345 350	1053

<210> 43

<211> 1082

<212> DNA
 <213> Human Immunodeficiency Virus (HIV)

<220>
 <221> CDS
 <222> (1)...(297)
 <223> HIV Protease

<221> CDS
 <222> (298)...(1082)
 <223> Portion of HIV Reverse Transcriptase

<400> 43

cct	caa	atc	act	ctt	tgg	caa	cga	ccc	ctt	gtc	aca	rta	aag	rta	ggg	48
Pro	Gln	Ile	Thr	Leu	Trp	Gln	Arg	Pro	Leu	Val	Thr	Xaa	Lys	Xaa	Gly	
1				5					10					15		
ggg	caa	cta	aag	gaa	gct	yta	ttr	gat	aca	gga	gca	gat	gat	aca	gta	96
Gly	Gln	Leu	Lys	Glu	Ala	Xaa	Xaa	Asp	Thr	Gly	Ala	Asp	Asp	Thr	Val	
			20					25					30			
tta	gaa	gaa	atg	aat	tta	cca	gga	aga	tgg	aaa	cca	aaa	atg	ata	ggg	144
Leu	Glu	Glu	Met	Asn	Leu	Pro	Gly	Arg	Trp	Lys	Pro	Lys	Met	Ile	Gly	
			35				40					45				
gga	att	gga	ggt	ttt	atc	aaa	gta	aga	cag	tat	gat	cag	ata	ccc	ata	192
Gly	Ile	Gly	Gly	Phe	Ile	Lys	Val	Arg	Gln	Tyr	Asp	Gln	Ile	Pro	Ile	
	50					55					60					
gaa	aty	tgt	ggg	cat	aaa	gct	ata	ggt	aca	gta	tta	gta	ggg	cct	aca	240
Glu	Xaa	Cys	Gly	His	Lys	Ala	Ile	Gly	Thr	Val	Leu	Val	Gly	Pro	Thr	
	65				70				75					80		
cct	gtc	aac	ata	att	gga	aga	aat	ttg	ttg	act	cag	att	ggt	tgc	act	288
Pro	Val	Asn	Ile	Ile	Gly	Arg	Asn	Leu	Leu	Thr	Gln	Ile	Gly	Cys	Thr	
				85					90					95		
tta	aat	ttt	cct	att	agt	cct	att	gaa	act	gta	cca	gta	aaa	tta	aag	336
Leu	Asn	Phe	Pro	Ile	Ser	Pro	Ile	Glu	Thr	Val	Pro	Val	Lys	Leu	Lys	
			100					105					110			
cca	gga	atg	gat	ggc	ccc	aaa	gtt	aaa	caa	tgg	cca	ttg	aca	gaa	gaa	384
Pro	Gly	Met	Asp	Gly	Pro	Lys	Val	Lys	Gln	Trp	Pro	Leu	Thr	Glu	Glu	
		115					120					125				
aaa	ata	aaa	gca	tta	gta	gaa	att	tgt	aca	gaa	atg	gaa	aaa	gaa	ggg	432
Lys	Ile	Lys	Ala	Leu	Val	Glu	Ile	Cys	Thr	Glu	Met	Glu	Lys	Glu	Gly	
	130					135					140					
aaa	att	tca	aaa	att	ggg	cct	gaa	aat	cca	tac	aat	act	cca	gta	ttt	480
Lys	Ile	Ser	Lys	Ile	Gly	Pro	Glu	Asn	Pro	Tyr	Asn	Thr	Pro	Val	Phe	
	145				150					155					160	
gcc	ata	aag	aaa	aag	gac	agt	act	aaa	tgg	aga	aaa	tta	gta	gat	ttc	528
Ala	Ile	Lys	Lys	Lys	Asp	Ser	Thr	Lys	Trp	Arg	Lys	Leu	Val	Asp	Phe	
				165					170					175		
aga	gaa	ctt	aat	aag	aga	act	caa	gac	ttt	tgg	gaa	gtt	caa	tta	gga	576
Arg	Glu	Leu	Asn	Lys	Arg	Thr	Gln	Asp	Phe	Trp	Glu	Val	Gln	Leu	Gly	
			180					185					190			
ata	ccg	cat	ccc	gca	ggg	tta	aaa	aag	aaa	aag	tca	gta	aca	gta	ctg	624
Ile	Pro	His	Pro	Ala	Gly	Leu	Lys	Lys	Lys	Lys	Ser	Val	Thr	Val	Leu	
		195					200					205				

gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg 210 215 220	672
aaa tat ast gca ttt acc ata ccg agt ata aac aat gag aca cca ggg Lys Tyr Xaa Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240	720
att aga tat cag tac aat gtg ctt ccg cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa tgt agc atg aca aaa atc tta gaa cct ttt aga aaa Ala Ile Phe Gln Cys Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gac ata gtt atc tat caa tac atg gat gat ttg tat gta Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac ttg gaa ata ggg cag cat aga aca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300	912
aga cag cat ctg ttg aaa tgg ggr ttt acc aca cca gac aag aaa cat Arg Gln His Leu Leu Lys Trp Xaa Phe Thr Thr Pro Asp Lys Lys His 305 310 315 320	960
cag aaa gaa cct cca ttc ctt tgg atg ggg tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta caa ccg ata gag ctg cca gaa aaa gaa agc tgg act Lys Trp Thr Val Gln Pro Ile Glu Leu Pro Glu Lys Glu Ser Trp Thr 340 345 350	1056
gtc aat gac ata cag aag tta gtg gg Val Asn Asp Ile Gln Lys Leu Val 355 360	1082

<210> 44
 <211> 1116
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)

<220>
 <221> CDS
 <222> (1)...(297)
 <223> HIV Protease

<221> CDS
 <222> (298)...(1116)
 <223> Portion of HIV Reverse Transcriptase

<400> 44 cct cag atc act ctt tgg caa cga ccc atc gtc aca gta aag ata ggg Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Val Lys Ile Gly 1 5 10 15	48
ggg caa cta aag gaa gct yta tta gat aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Xaa Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30	96

tta gaa gaa atg aat tta cca gga aaa tgg aaa cca aaa ata ata ggg Leu Glu Glu Met Asn Leu Pro Gly Lys Trp Lys Pro Lys Ile Ile Gly	144
35 40 45	
gga att gga ggt ttt gcc aaa gta aga cag tat gat cag ata ccc ata Gly Ile Gly Gly Phe Ala Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile	192
50 55 60	
gaa atc tka gga cat aaa gtt ata ggt aca gtc tta gta gga cct aca Glu Ile Xaa Gly His Lys Val Ile Gly Thr Val Leu Val Gly Pro Thr	240
65 70 75 80	
cct gcc aac ata att gga aga aat ctg ttg act cag att ggt tgc act Pro Ala Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr	288
85 90 95	
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys	336
100 105 110	
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu	384
115 120 125	
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa gga Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly	432
130 135 140	
aaa att tca aag att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe	480
145 150 155 160	
gcc ata aag aaa aaa aac agy act wga tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asn Xaa Thr Xaa Trp Arg Lys Leu Val Asp Phe	528
165 170 175	
aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa ttr gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Xaa Gly	576
180 185 190	
ata cca cat ccc tca ggg tta aaa aag aam aaa tca gta aca gta ctg Ile Pro His Pro Ser Gly Leu Lys Lys Xaa Lys Ser Val Thr Val Leu	624
195 200 205	
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg	672
210 215 220	
aaa tat act gca ttt acc ata cct agt rta aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Xaa Asn Asn Glu Thr Pro Gly	720
225 230 235 240	
att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro	768
245 250 255	
gca ata ttc caa agt agc atg aca aga atc cta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Arg Ile Leu Glu Pro Phe Arg Lys	816
260 265 270	
cag aat cca gac ata gtt atc tat caa tac gtg gat gac ttg ctt gta Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Leu Val	864
275 280 285	

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gga tct gat tta gaa ata ggg caa cat aga gca aaa ata gag gaa ctg      912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Leu
  290                295                300

aga caa cat ctg ttg agg tgg ggg ttt atc aca cca gac gaa aaa cat      960
Arg Gln His Leu Leu Arg Trp Gly Phe Ile Thr Pro Asp Glu Lys His
  305                310                315                320

cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat      1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
                325                330                335

aaa tgg aca gta cag ccc ata gtg ctg cca gaa aaa gay agc tgg act      1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
                340                345                350

gtc aat gac ata caa aag tta gtg gga aaa ttg aat tgg gca agc cag      1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
                355                360                365

att tat gca ggg
Ile Tyr Ala Gly
  370
      1116

<210> 45
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

<400> 45
cct cag atc act ctt tgg caa cga ccc rtc gtc aca ata aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Xaa Val Thr Ile Lys Ile Gly
  1                5                10                15

ggg cag cta aag gaa gct cta tta gat aca gga gca gac gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
                20                25                30

tta gaa gaa atg aat tta cca gga aaa tgg aaa cca aaa atg ata gtg      144
Leu Glu Glu Met Asn Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Val
                35                40                45

gga att gga gga ttt gtc aaa gta aaa cag tat gag caa ata cct gta      192
Gly Ile Gly Gly Phe Val Lys Val Lys Gln Tyr Glu Gln Ile Pro Val
  50                55                60

gaa atc tgt gga cat aaa gct gta ggt aca gta tta gta gga cct aca      240
Glu Ile Cys Gly His Lys Ala Val Gly Thr Val Leu Val Gly Pro Thr
  65                70                75                80

cct gcc aac ata att gga aga aat ctg ttg act cag att ggt tgc act      288
Pro Ala Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
                85                90                95

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tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca aaa gar Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Lys Glu 115 120 125	384
aaa ata maa gca ttg gta gaa att tgt aca gaa atg gaa aag gaa gga Lys Ile Xaa Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly 130 135 140	432
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gtg ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gct ata aag aaa aag aac agt gat aga tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asn Ser Asp Arg Trp Arg Lys Leu Val Asp Phe 165 170 175	528
aga gaa ctt aat aag agg act caa gac ttc tgg gaa att caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Ile Gln Leu Gly 180 185 190	576
ata cca cat ccc gca ggg tta aaa aag aag aaa tca gta aca rta cta Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Xaa Leu 195 200 205	624
gat gtg ggt gat gca tat ttt tca rtt ccc tta gat aaa gaa ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Xaa Pro Leu Asp Lys Glu Phe Arg 210 215 220	672
aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240	720
att aga tat caa tac aat gtg ctt cca caa gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa gct agc atg aca aaa atc tta gag cct ttc aga aaa Ala Ile Phe Gln Ala Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gaa cta gtt atc tat caa tac gtg gat gac ttg tat gta Gln Asn Pro Glu Leu Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac tta gaa ata gga cag cat aga aca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300	912
aga gaa cat ctg tta aaa tgg gga tta ttc aca cca gac cag aaa cat Arg Glu His Leu Leu Lys Trp Gly Leu Phe Thr Pro Asp Gln Lys His 305 310 315 320	960
cag aaa gaa ccc cca ttt ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg act ata cag cct atg gtg ctg cca gaa aaa gac agc tgg act Lys Trp Thr Ile Gln Pro Met Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056


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gtc aat gac cta cag aag tta gtg gga aaa ttg aat tgg gca agt cag      1104
Val Asn Asp Leu Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
      355                      360                      365

att tat cca ggg      1116
Ile Tyr Pro Gly
      370

<210> 46
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

<400> 46
cct caa atc act ctt tgg caa cga ccc ctc gtc aca ata aaa gta ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Val Gly
      1                      5                      10                      15

ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
      20                      25                      30

tta gaa gaa atg aat ttg cca gga agg tgg aaa cca aaa atg ata ggg      144
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
      35                      40                      45

gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata tcc ata      192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Ser Ile
      50                      55                      60

gaa atc tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca      240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr
      65                      70                      75                      80

cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act      288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
      85                      90                      95

tta aat ttt cct att agt cct att gaa act gta cca gta aaa tta aag      336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
      100                      105                      110

cca gga atg gac ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa      384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
      115                      120                      125

aaa ata aaa gca tta gta gag att tgt aca gaa atg gaa aag gaa gga      432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
      130                      135                      140

aaa att tca aaa att ggg cct gaa aac cca tac aat act cca gta ttt      480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
      145                      150                      155                      160

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gcc ata aag aaa aaa gac agt act aag tgg aga aaa tta gta gat ttc 528
Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
165 170 175

aga gaa ctt aat aaa aga act caa gac ttc tgg gag gtt caa tta gga 576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
180 185 190

ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta cta 624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu
195 200 205

gat gtg ggc gat gca tat ttc tca gtt ccc tta gat gaa gac ttc aga 672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg
210 215 220

aaa tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg 720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly
225 230 235 240

act aga tat cag tac aat gtg ctc cca cag gga tgg aaa gga tca cca 768
Thr Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
245 250 255

gca ata ttc caa tgt agc atg aca aaa atc tta gag cct ttt aga aaa 816
Ala Ile Phe Gln Cys Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys
260 265 270

caa aat cca gac cta gtt atc tat caa tac atg gat gat ttg tat gta 864
Gln Asn Pro Asp Leu Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val
275 280 285

gga tct gac tta gaa ata gga cag cat aga aca aaa ata gag gaa ctg 912
Gly Ser Asp Leu Glu Ile Gln His Arg Thr Lys Ile Glu Glu Leu
290 295 300

aga caa cat ctg ttg agg tgg gga ttt acc acc cca gac aaa aaa cat 960
Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His
305 310 315 320

cag aaa gaa cct cca ttt ctt tgg atg ggt tat gaa ctc cat cct gat 1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
325 330 335

aaa tgg aca gtr cag cct ata gtg ctg cca gaa aaa gac agc tgg act 1056
Lys Trp Thr Xaa Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
340 345 350

gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag 1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
355 360 365

att tac cca ggg 1116
Ile Tyr Pro Gly
370

<210> 47
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)
<220>

<221> CDS
 <222> (1)...(297)
 <223> HIV Protease

<221> CDS
 <222> (298)...(1116)
 <223> Portion of HIV Reverse Transcriptase

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<400> 47
cct caa atc act ctt tgg caa cga ccc ctc gtc aca gta aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Val Lys Ile Gly
  1             5             10             15

ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
             20             25             30

tta gaa gac atg tgt ttg cca gga aga tgg aaa cca aaa atg ata ggg      144
Leu Glu Asp Met Cys Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
             35             40             45

gga att gga ggt ttt atc aaa gta aga caa tat gat cag gta gcc atg      192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Val Ala Met
  50             55             60

gaa atc tgt gga cat aag gct ata ggt aca gta tta ata gga cct aca      240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Ile Gly Pro Thr
  65             70             75             80

cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act      288
Pro Val Asn Ile Ile Gly Arg Asn Leu Thr Gln Ile Gly Cys Thr
             85             90             95

tta aat ttt ccc att agc cct att gaa act gta ccm gta aaa tta aag      336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Xaa Val Lys Leu Lys
             100            105            110

cca ggr atg gat ggt cca agg gtt aaa caa tgg cca ttg aca gaa gaa      384
Pro Xaa Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu
             115            120            125

aaa ata ara gca tta gta gaa att tgt aca gaa atg gaa aag gaa gga      432
Lys Ile Xaa Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
             130            135            140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt      480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
             145            150            155            160

gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttt      528
Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
             165            170            175

aga gaa ctt aat aag aaa act caa gac tty tgg gaa gtt caa tta ggr      576
Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Xaa
             180            185            190

ata ccg cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta ctt      624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu
             195            200            205

gat gtg gga gat gca tat ttt tca gtt ccc tta gat aaa gat ttc agg      672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg
             210            215            220

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aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg 720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly
225 230 235 240

att aga tat caa tac aat gtg ctt cca cag gga tgg aaa gga tca cca 768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
245 250 255

gca ata ttc caa agt agc atg aca aaa att tta gag cct ttt aga aag 816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys
260 265 270

caa aat cca gac ata gtt atc tat caa tac gtg gat gat ttg tat gta 864
Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val
275 280 285

gga tct gac tta gaa ata gga cag cat aga aca aaa ata gag gaa ctr 912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Xaa
290 295 300

aga caa cat ctg ttg aag tgg ggg ytt acc aca cca gac aag aaa cat 960
Arg Gln His Leu Leu Lys Trp Gly Xaa Thr Thr Pro Asp Lys Lys His
305 310 315 320

cag aaa gaa ccy cca ttc ctt tgg atg ggk tat gaa ctc cat cct gat 1008
Gln Lys Glu Xaa Pro Phe Leu Trp Met Xaa Tyr Glu Leu His Pro Asp
325 330 335

aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act 1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
340 345 350

gtc aat gac ata cag aag tta gtg gga aar ttg aat tgg gca agt cag 1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
355 360 365

att tat gca ggg 1116
Ile Tyr Ala Gly
370

<210> 48
<211> 1115
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1115)
<223> Portion of HIV Reverse Transcriptase

<400> 48
cct cag atc act ctt tgg caa cga ccc ctc gtc aca gta aag ata ggg 48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Val Lys Ile Gly
1 5 10 15

ggg cag cta aag gaa gct cta tta gat aca gga gca gat gat aca gta 96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
20 25 30

ata gaa gac ata gaa ttg cca gga aga tgg aaa cca aaa atg ata ggg Ile Glu Asp Ile Glu Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly 35 40 45	144
gga att gga ggt ttt atc aaa gta aaa cag tat gag cag gta ccc ata Gly Ile Gly Gly Phe Ile Lys Val Lys Gln Tyr Glu Gln Val Pro Ile 50 55 60	192
gaa ctc tgt ggg cgt aaa act ata ggt aca gta tta gta gga cct aca Glu Leu Cys Gly Arg Lys Thr Ile Gly Thr Val Leu Val Gly Pro Thr 65 70 75 80	240
cct gtc aac ata att gga aga aac ctg atg act cag att ggt tgc act Pro Val Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Ile Gly Cys Thr 85 90 95	288
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta ata gaa att tgt aca gaa atg gaa aag gaa ggg Lys Ile Lys Ala Leu Ile Glu Ile Cys Thr Glu Met Glu Lys Glu Gly 130 135 140	432
aaa att tca aaa att ggg cct gaa aat cca tac aac act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gcy ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc Xaa Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528
aga gaa ctt aat aag aaa act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat cct gca ggg tta aaa aag aag aaa tca gta aca gta ttg Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtt ccg tta gat aaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg 210 215 220	672
aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240	720
att aga tat cag tac aat gtg ctk cca cag gga tgg aag gga tca cca Ile Arg Tyr Gln Tyr Asn Val Xaa Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agt agc atg aca aaa atc ttg gag ccc ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gac cta gtt atc tat caa tac atg gat gat ttg tat gta Gln Asn Pro Asp Leu Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864

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ggc tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg      912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu
290                               295                               300

aga caa cat ctg ttg aag tgg gga ttt acc aca cca gat aaa aaa cat      960
Arg Gln His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His
305                               310                               315                               320

cag aaa gaa cct cca ttt ctt tgg atg ggt tat gaa ctc cat cct gat      1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
325                               330                               335

aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act      1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
340                               345                               350

gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag      1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
355                               360                               365

att tcc car ga      1115
Ile Ser Gln
370

<210> 49
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

<400> 49
cct cag atc act ctt tgg caa cga ccc ctc gtc rca ata aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Xaa Ile Lys Ile Gly
1                               5                               10                               15

ggg cag cta aag gaa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
20                               25                               30

tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aag atg ata ggg      144
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
35                               40                               45

gga att gga ggt ttc atc aaa gta aga cag tat gat cag ata ccc ata      192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile
50                               55                               60

gaa atc tgt ggc cat aaa gct ata ggt aca gta tta gta gga cct aca      240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr
65                               70                               75                               80

cct gtc aac ata att gga aga aat cta ttg act cag att ggt tgc act      288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
85                               90                               95

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tta aat ttt ccc att agt cct att gaa act gta cca gta aag tta aag	336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys	
100 105 110	
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa	384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu	
115 120 125	
aaa ata aaa gca tta gta gaa atc tgt aca gaa atg gaa aag gaa ggg	432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly	
130 135 140	
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt	480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe	
145 150 155 160	
gcc ata aag aaa aag gac agt act aaa tgg aga aaa tta gta gat ttc	528
Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe	
165 170 175	
aga gaa ctt aat aag aaa act caa gac ttc tgg gaa gtt caa tta gga	576
Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Gly	
180 185 190	
ata cca cat cct gca ggg tta aaa aag aam aaa tca gta aca gta ctg	624
Ile Pro His Pro Ala Gly Leu Lys Xaa Lys Ser Val Thr Val Leu	
195 200 205	
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gaa ttc agg	672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Glu Phe Arg	
210 215 220	
aag tat acc gca ttt cca tcc cta gtt ata aac aat gag aca cca gga	720
Lys Tyr Thr Ala Phe Pro Ser Leu Val Ile Asn Asn Glu Thr Pro Gly	
225 230 235 240	
atc aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca	768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro	
245 250 255	
gca ata ttt caa agt agc atg aca aaa atc tta gag cct ttt aga aaa	816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys	
260 265 270	
caa aat cca gac ata gtt atc tat caa tac gtg gat gat ttg tat gta	864
Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val	
275 280 285	
gga tct gac tta gaa ata ggg cag cat aga aca aaa gta gag gag ctg	912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Val Glu Glu Leu	
290 295 300	
aga caa cat ctg ttg agg tgg gga ttt acc aca cca gac aaa aaa cat	960
Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His	
305 310 315 320	
cag aaa gag cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat	1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp	
325 330 335	
aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act	1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr	
340 345 350	

gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agc cag 1104
 Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
 355 360 365

att tac cca ggg 1116
 ile tyr pro gly
 370

<210> 50
 <211> 1116
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)

<220>
 <221> CDS
 <222> (1)...(297)
 <223> HIV Protease

<221> CDS
 <222> (298)...(1116)
 <223> Portion of HIV Reverse Transcriptase

<400> 50
 cct cag atc act ctt tgg caa cga ccc ttc gtc aac ata aag ata ggg 48
 Pro Gln ile Thr Leu Trp Gln Arg Pro Phe Val Asn ile Lys ile Gly
 1 5 10 15

gga caa ctg aag gaa gct cta ttg gat aca gga gca gat gat aca gta 96
 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
 20 25 30

tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa ttg ata ggg 144
 Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Leu ile Gly
 35 40 45

gga att gga ggt ttk gtc aaa gta aga cag tat gat cag ata cct gta 192
 Gly ile Gly Gly Xaa Val Lys Val Arg Gln Tyr Asp Gln ile Pro Val
 50 55 60

gaa att tgt gga cat aaa gyt ata ggt aca gtc tta gta gga cct aca 240
 Glu ile Cys Gly His Lys Xaa ile Gly Thr Val Leu Val Gly Pro Thr
 65 70 75 80

cct gcc aac ata att gga aga aat ctg ttg act cag att ggc tgc act 288
 Pro Ala Asn ile ile Gly Arg Asn Leu Leu Thr Gln ile Gly Cys Thr
 85 90 95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336
 Leu Asn Phe Pro ile Ser Pro ile Glu Thr Val Pro Val Lys Leu Lys
 100 105 110

cca gga atg gat ggc ccg aga gtt aaa caa tgg cca ttg aca gaa gaa 384
 Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu
 115 120 125

aaa ata aaa gca tta gta gaa att tgt aca gaa ttg gaa aag gaa gga 432
 Lys ile Lys Ala Leu Val Glu ile Cys Thr Glu Leu Glu Lys Glu Gly
 130 135 140

aaa att tca aag att ggg cct gaa aat cca tac aat act cca ata ttt 480
 Lys ile Ser Lys ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro ile Phe
 145 150 155 160

gcc ata aag aaa aag aac agt act aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asn Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528
aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat ccc gca ggg tta mam aag aac aaa tca gta aca gtg cta Ile Pro His Pro Ala Gly Leu Xaa Lys Asn Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtt ccc tta tat gaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Tyr Glu Asp Phe Arg 210 215 220	672
aag tat act gca ttt acc ata cct agt aca aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly 225 230 235 240	720
att aga tat cag tay aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc cag agt agc atg aca aga atc tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Arg Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gaa ata gtc atc tat caa tac gtg gat gat ttg tat gta Gln Asn Pro Glu Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val 275 280 285	864
gca tct gac tta gaa ata gag aaa cat aga aca aaa ata gag gaa ctg Ala Ser Asp Leu Glu Ile Glu Lys His Arg Thr Lys Ile Glu Glu Leu 290 295 300	912
aga caa cat ctg ttg agg tgg gga ttt tac aca cca gac aaa aag cat Arg Gln His Leu Leu Arg Trp Gly Phe Tyr Thr Pro Asp Lys Lys His 305 310 315 320	960
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056
gtc aat gac ata cag aaa tta gtg gga aaa ttg aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
att tat gga ggg Ile Tyr Gly Gly 370	1116

<210> 51
 <211> 1116
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)

<220>

<221> CDS
 <222> (1)...(297)
 <223> HIV Protease

<221> CDS
 <222> (298)...(1116)
 <223> Portion of HIV Reverse Transcriptase

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<400> 51
cct cag atc act ctt tgg caa cga ccc atc gtc aca ata aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Ile Gly
  1             5             10             15

ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
             20             25             30

tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa ata ata ggg     144
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Ile Ile Gly
             35             40             45

gga att gga ggt ttt aty aaa gta aga cag tat gat cag ata cct ata     192
Gly Ile Gly Gly Phe Xaa Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile
             50             55             60

gaa atc tgt gga cat aaa act ata ggt aca gta tta ata gga cct aca     240
Glu Ile Cys Gly His Lys Thr Ile Gly Thr Val Leu Ile Gly Pro Thr
             65             70             75

cct gcc aac ata att gga aga gat ctg ttg act cag att ggt tgc act     288
Pro Ala Asn Ile Ile Gly Arg Asp Leu Leu Thr Gln Ile Gly Cys Thr
             85             90             95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa ttg aag     336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
             100            105            110

cca gga atg gat ggt cca aaa gtt aaa caa tgg cca ttg aca gaa gaa     384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
             115            120            125

aaa ata aaa gca tta gta gaa att tgt aca gaa ctg gaa aag gat ggg     432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Asp Gly
             130            135            140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cct gta ttt     480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
             145            150            155

gcc ata aag aaa aaa aac agt act aaa tgg aga aaa tta gta gat ttc     528
Ala Ile Lys Lys Lys Asn Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
             165            170            175

aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga     576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
             180            185            190

ata cca cat ccc gcg ggg tta aaa aag aaa aaa tca gta aca gta ctg     624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu
             195            200            205

gat gtg ggt gat gca tat ttt tca att ccc tta gat gaa gaa ttc agg     672
Asp Val Gly Asp Ala Tyr Phe Ser Ile Pro Leu Asp Glu Glu Phe Arg
             210            215            220

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aag tat act gca ttc acc ata cct agt ata aac aat gag aca cca ggg      720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly
225                               230                               235                               240

gtt aga tat caa tac aat gtg ctt cca cag gga tgg aaa gga tca cca      768
Val Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
                               245                               250                               255

gca ata ttc caa agt agc atg aca aaa atc tta gag ccc ttt aga aaa      816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys
                               260                               265                               270

caa aat cca gac ata gtt atc tat caa tat gtg gat gat ttg tat gta      864
Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val
                               275                               280                               285

gga tct gac tta gaa ata ggg cag cat aga gca aaa ata gag gaa ctg      912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Leu
                               290                               295                               300

aga caa cat ctg tgg agg tgg ggg ttt tac aca cca gac aaa aaa cat      960
Arg Gln His Leu Trp Arg Trp Gly Phe Tyr Thr Pro Asp Lys Lys His
305                               310                               315                               320

cag aaa gaa ccc cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat      1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
                               325                               330                               335

aaa tgg aca gta caa cct ata gtg ctg cca gaa aaa gac agc tgg act      1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
                               340                               345                               350

gtc aat gac ata cag aaa tta gtg ggg aaa ttg aat tgg gca agt cag      1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
                               355                               360                               365

att tat gca ggg
Ile Tyr Ala Gly
370

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<210> 52
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

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<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

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<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

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<400> 52
cct caa atc act ctt tgg caa cga ccc ctt gtc aca ata aag rta ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Xaa Gly
1 .                               5                               10                               15

ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
                               20                               25                               30

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tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atr ata ggg Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Xaa Ile Gly 35 40 45	144
gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ycc ata Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Xaa Ile 50 55 60	192
gaa atc tgt gga cat aaa gct ata ggt tca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Ala Ile Gly Ser Val Leu Val Gly Pro Thr 65 70 75 80	240
cct gtc aac ata aty gga aga aat ctg atg act cag att ggt tgc act Pro Val Asn Ile Xaa Gly Arg Asn Leu Met Thr Gln Ile Gly Cys Thr 85 90 95	288
tta aat ttt ccc att agt cct att gaa ack gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Xaa Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtt aag caa tgg cca ttg aca gra gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Xaa Glu 115 120 125	384
aaa ata aaa gca tta gta gaa att tgt aca gag atg gaa aag gaa ggg Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly 130 135 140	432
aaa att tca aga att ggg ccc gaa aat cca tac aat act cca ata ttt Lys Ile Ser Arg Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe 145 150 155 160	480
gcc ata aag aaa aag aat agt act aga tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asn Ser Thr Arg Trp Arg Lys Leu Val Asp Phe 165 170 175	528
agg gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat ccc gca ggg tta aaa aag aac aaa tca gtg aca gta ytg Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Xaa 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat gaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg 210 215 220	672
aag tat act gca ttt acc ata cct agt atr aac aat gag aaa cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Xaa Asn Asn Glu Lys Pro Gly 225 230 235 240	720
att aga tat cag tac aat gtg ctt cca car gga tgg aaa ggg tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa tgt agc atg aca aaa aty tta gag cct ttt aga aaa Ala Ile Phe Gln Cys Ser Met Thr Lys Xaa Leu Glu Pro Phe Arg Lys 260 265 270	816
car aat cca gac ata gtt atc tat caa tac atg gat gat ttg tat gta Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864

gga tct gac tta gaa ata gaa cag cat aga aca aaa ata gag gaa ttg 912
 Gly Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Glu Glu Leu
 290 295 300

aga caa cat ctg tta agg tgg gga ttt ttc aca cca gaa caa aaa cat 960
 Arg Gln His Leu Leu Arg Trp Gly Phe Phe Thr Pro Glu Gln Lys His
 305 310 315 320

cag aaa gaa ccg cca ttc ctt tgg atg ggt tat gaa cta cat cct gat 1008
 Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
 325 330 335

aaa tgg acg gta cag cct ata aag ctg cca gaa aaa gat agc tgg act 1056
 Lys Trp Thr Val Gln Pro Ile Lys Leu Pro Glu Lys Asp Ser Trp Thr
 340 345 350

gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt cag 1104
 Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
 355 360 365

att tay gca ggg 1116
 Ile Tyr Ala Gly
 370

<210> 53
 <211> 1116
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)

<220>
 <221> CDS
 <222> (1)...(297)
 <223> HIV Protease

<221> CDS
 <222> (298)...(1116)
 <223> Portion of HIV Reverse Transcriptase

<400> 53
 cct cag atc act ctt tgg caa cga ccc atc gtc aca ata aag ata ggg 48
 Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Ile Gly
 1 5 10 15

ggg caa cta aaa gaa gct cta tta gat aca gga gca gat gat aca gta 96
 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
 20 25 30

tta gaa gaa atg aat tta cca gga aga tgg aaa cca aaa atg ata ggg 144
 Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
 35 40 45

gga att gga ggt ttt atc aaa gtg aga cag tat gat cag rta ccc ata 192
 Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Xaa Pro Ile
 50 55 60

gaa att tgt gga cat aaa gct ata ggt aca gta tta gta gga tct aca 240
 Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Ser Thr
 65 70 75 80

cct gtc aac ata att gga aga aat ctg ttg act cag ctt ggg tgc act 288
 Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr
 85 90 95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag	336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys	
100 105 110	
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa	384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu	
115 120 125	
aaa ata aaa gca tta gta gaa att tgt aca gag atg gaa aag gaa ggg	432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly	
130 135 140	
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt	480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe	
145 150 155 160	
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc	528
Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe	
165 170 175	
aga gaa ctt aat aag aaa act caa gac ttc tgg gaa gtt caa tta gga	576
Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Gly	
180 185 190	
atc cca cat cct gca ggg tta aaa aag aaa aaa tca gta aca gta ctg	624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu	
195 200 205	
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc cgg	672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg	
210 215 220	
aag tat act gca ttt acc ata cct agt aca aac aat gag aca cca gga	720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly	
225 230 235 240	
att aga tat cag tac aat gtg ctt cca caa gga tgg aaa gga tca cca	768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro	
245 250 255	
gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt agg aat	816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Asn	
260 265 270	
aaa aat cca gac ata gtt atc tat caa tac gtg gat gat ttg tat gta	864
Lys Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val	
275 280 285	
gga tct gac cta gaa ata ggg cag cat aga gca aaa ata gag gaa ctg	912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Leu	
290 295 300	
aga gaa cat ctg ttg aag tgg ggg ttt act aca cca gac aaa aaa cat	960
Arg Glu His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His	
305 310 315 320	
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat	1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp	
325 330 335	
aaa tgg aca gtc cag cct ata gag ctg cca gaa aaa gac agc tgg act	1056
Lys Trp Thr Val Gln Pro Ile Glu Leu Pro Glu Lys Asp Ser Trp Thr	
340 345 350	

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gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag      1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
      355                      360                      365

att tat gca gga
Ile Tyr Ala Gly
      370

<210> 54
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

<400> 54
cct cag atc act ctt tgg caa cga ccc aty gtc aca ata aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Xaa Val Thr Ile Lys Ile Gly
      1                      5                      10                      15

ggg caa cta aag gaa gct yta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Xaa Leu Asp Thr Gly Ala Asp Asp Thr Val
      20                      25                      30

tta gaa gac atg gat ttg cca gga aga tgg aaa cca aaa atg ata gtg      144
Leu Glu Asp Met Asp Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Val
      35                      40                      45

gga att gga ggt ttt gtc aaa gta aga cag tat gat cag ata ccc ata      192
Gly Ile Gly Gly Phe Val Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile
      50                      55                      60

gaa atc tgt gga cat aaa att ata ggt aca gta tta ata gga aat aca      240
Glu Ile Cys Gly His Lys Ile Ile Gly Thr Val Leu Ile Gly Asn Thr
      65                      70                      75                      80

cct gcc aac gta att gga aga aat ctg ttg act cag ctt ggt tgc act      288
Pro Ala Asn Val Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr
      85                      90                      95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag      336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
      100                      105                      110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa      384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
      115                      120                      125

aaa ata aaa gca tta gta gaa att tgt aca gaa ctg gaa aag gat ggg      432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Asp Gly
      130                      135                      140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt      480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
      145                      150                      155                      160

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gcc ata aag aaa aag gac agt act aaa tgg aga aaa gta gta gat ttc Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Val Val Asp Phe 165 170 175	528
aga gaa ctt aac aag aga act caa gac ttc tgg gag gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cac ccc gca ggg ata aaa aag aat aaa tca gta act gta cta Ile Pro His Pro Ala Gly Ile Lys Lys Asn Lys Ser Val Thr Val Leu 195 200 205	624
gat gta ggt gat gca tat ttc tca gtt ccc tta gat gaa gac ttc aga Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg 210 215 220	672
aaa tat act gca ttc acc ata cct agt att aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240	720
att aga tat cag tac aat gtg ctc cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gac ata gtt atc tat caa tac atg gat gat ttg tat gta Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac tta gaa ata ggg cag cac aga ata aaa ata rag gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ile Lys Ile Xaa Glu Leu 290 295 300	912
aga gaa cat cta tgg aag tgg gga ttt tac aca cca gac aaa aag cat Arg Glu His Leu Trp Lys Trp Gly Phe Tyr Thr Pro Asp Lys Lys His 305 310 315 320	960
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta cag cct ata acg ctg cca gaa aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Thr Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056
gtc aat gac ata cag aag tta gtg ggg aaa ttg aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
att tat gca ggg Ile Tyr Ala Gly 370	1116

<210> 55

<211> 1116

<212> DNA

<213> Human Immunodeficiency Virus (HIV)

<220>

<221> CDS
 <222> (1)...(297)
 <223> HIV Protease

<221> CDS
 <222> (298)...(1116)
 <223> Portion of HIV Reverse Transcriptase

<400> 55
 cct caa atc act ctt tgg caa cga ccc ctc gtc gca ata aag ata ggg 48
 Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Ala Ile Lys Ile Gly
 1 5 10 15

ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gtc 96
 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
 20 25 30

tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atg ata ggg 144
 Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
 35 40 45

gga att gga ggt ttt atc aaa gta aag cag tat gat cag gta ctt gta 192
 Gly Ile Gly Gly Phe Ile Lys Val Lys Gln Tyr Asp Gln Val Leu Val
 50 55 60

gaa att tgt gga cat ara gct ata ggt aca gta tta gta gga cct aca 240
 Glu Ile Cys Gly His Xaa Ala Ile Gly Thr Val Leu Val Gly Pro Thr
 65 70 75 80

cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgt act 288
 Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
 85 90 95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
 100 105 110

cca ggt atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
 115 120 125

aaa ata aaa gca tta ata gaa att tgt aca gaa atg gaa aag gaa ggg 432
 Lys Ile Lys Ala Leu Ile Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
 130 135 140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt 480
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
 145 150 155 160

gcc ata aag aaa aaa gac agt acc aaa tgg aga aaa tta gta gat ttc 528
 Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
 165 170 175

aga gaa ctt aat aag aaa acg caa gac ttc tgg gaa gtt caa tta gga 576
 Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
 180 185 190

ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta ctg 624
 Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu
 195 200 205

gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aag gac ttc agg 672
 Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg
 210 215 220

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aag tat act gca ttt acc ata cct agt gta aac aat gag aca cca ggg      720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Val Asn Asn Glu Thr Pro Gly
225                               230                               235                               240

att aga tat cag tac aat gtg ctg cca cag gga tgg aaa gga tca cca      768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
                               245                               250                               255

gca ata ttt caa agt agc atg aca aaa atc tta gag cct ttt aga aaa      816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys
                               260                               265                               270

caa aat cca gac atg gtt atc tat caa tac atg gat gat ttg tat gta      864
Gln Asn Pro Asp Met Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val
                               275                               280                               285

gga tct gac tta gaa ata gag cag cat aga rca aaa ata gag gaa ctg      912
Gly Ser Asp Leu Glu Ile Glu Gln His Arg Xaa Lys Ile Glu Glu Leu
                               290                               295                               300

agg cag cat ctg ttg agg tgg gga ttt acc aca cca gac aaa aag cat      960
Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His
305                               310                               315                               320

cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat     1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
                               325                               330                               335

aaa tgg aca gta cag cct ata ktg ctg cca gaa aaa gac agc tgg act     1056
Lys Trp Thr Val Gln Pro Ile Xaa Leu Pro Glu Lys Asp Ser Trp Thr
                               340                               345                               350

gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt cag     1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
                               355                               360                               365

att tam ccc ngg
Ile Xaa Pro Xaa
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<210> 56
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

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<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

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<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

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<400> 56
cct caa atc act ctt tgg caa cga ccc att gtc aca ata aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Ile Gly
  1                               5                               10                               15

ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
                               20                               25                               30

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tta gaa gaa atg aat ttg cca gga aaa tgg aaa cca aaa atg ata ggg Leu Glu Glu Met Asn Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly	144
gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata acc ata Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Thr Ile	192
gaa atc tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr	240
cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr	288
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys	336
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu	384
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aaa gaa ggg Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly	432
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe	480
gcc ata aag aaa aaa gat agt act aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe	528
aga gaa ctt aat aag aga act caa gac ttc tgg gaa gta caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly	576
ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta cta Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu	624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gaa ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Glu Phe Arg	672
aag tat act gca ttc acc ata cct agt ata aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly	720
att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro	768
gca ata ttc caa agc agc atg aca aaa att tta gaa cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys	816
caa aat cca gaa ata gtt atc tat caa tac atg gat gat ttg tat gta Gln Asn Pro Glu Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val	864

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gga tct gac tta raa ata gag cag cat aga aca aaa ata gag gaa ctg      912
Gly Ser Asp Leu Xaa Ile Glu Gln His Arg Thr Lys Ile Glu Glu Leu
290                               295                               300

aga caa cat ctg ttg agg tgg gga ttt acc aca cca gac aaa aag cat      960
Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His
305                               310                               315                               320

cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat      1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
                               325                               330                               335

aaa tgg aca gta cag cct ata gtg ctg cca gaa cag gac agc tgg act      1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Gln Asp Ser Trp Thr
                               340                               345                               350

gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt cag      1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
                               355                               360                               365

att tat cca ggg
Ile Tyr Pro Gly
370

<210> 57
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

<400> 57
cct cag atc act ctt tgg caa cga ccc ctc gtc aca gta aag tta ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Val Lys Leu Gly
1                               5                               10                               15

ggg caa cta atg gaa gtt cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Met Glu Val Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
                               20                               25                               30

rta gaa gaa ata agt tta cca gga aga tgg aaa cca aaa atg ata ggg      144
Xaa Glu Glu Ile Ser Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
                               35                               40                               45

gga att gga ggt ttt gtc aaa gta aaa cag tat gat cag gta ccc tta      192
Gly Ile Gly Gly Phe Val Lys Val Lys Gln Tyr Asp Gln Val Pro Leu
50                               55                               60

gaa att tgt gga aaa aag gct ata ggt aca gta tta gta gga cct aca      240
Glu Ile Cys Gly Lys Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr
65                               70                               75                               80

cct gcc aac ata att gga aga aat ttt ttg gct cag att ggt tgc act      288
Pro Ala Asn Ile Ile Gly Arg Asn Phe Leu Ala Gln Ile Gly Cys Thr
                               85                               90                               95

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tta aat ttc ccc att agt cct att gaa act gta cca gta aaa tta aag	336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys	
100 105 110	
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa	384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu	
115 120 125	
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa ggg	432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly	
130 135 140	
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt	480
Lys Ile Ser Lys Ile ggg cct gaa aat cca tac aat act cca gta ttt	
145 150 155 160	
gcc ata aag aaa aag aac agt act aga tgg aga aaa tta gta gat ttt	528
Ala Ile Lys Lys Lys Asn Ser Thr Arg Trp Arg Lys Leu Val Asp Phe	
165 170 175	
aga gaa ctt aat aag agg acs caa gac ttc tgg gaa gtt caa tta gga	576
Arg Glu Leu Asn Lys Arg Xaa Gln Asp Phe Trp Glu Val Gln Leu Gly	
180 185 190	
ata cca cat ccc gca ggg tta aar aag aac aaa tca gta aca gta ctg	624
Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu	
195 200 205	
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat cca gac ttc agg	672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Pro Asp Phe Arg	
210 215 220	
aag tat act gca ttt acc ata cct agt aca aac aat gag aca cca ggg	720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly	
225 230 235 240	
att aga tat cag tac aat gtg ctt cca caa gga tgg aaa gga tca cca	768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro	
245 250 255	
gca ata ttc caa agt agc atg aca aaa atc tta gag cca ttt aga aaa	816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys	
260 265 270	
caa aat cca gac ata gtt atc tgt caa tac atg gat gat ttg tat gta	864
Gln Asn Pro Asp Ile Val Ile Cys Gln Tyr Met Asp Asp Leu Tyr Val	
275 280 285	
gga tct gac tta gaa ata gag cag cat aga aca aaa ata gag gaa ctg	912
Gly Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Glu Glu Leu	
290 295 300	
aga caa cat ctg ttg agg tgg gga ttt tac aca cca gac caa aaa cat	960
Arg Gln His Leu Leu Arg Trp Gly Phe Tyr Thr Pro Asp Gln Lys His	
305 310 315 320	
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat	1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp	
325 330 335	
aaa tgg aca gta cag cct ata acg ctg cca gac aaa gac agc tgg act	1056
Lys Trp Thr Val Gln Pro Ile Thr Leu Pro Asp Lys Asp Ser Trp Thr	
340 345 350	

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gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt cag      1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
      355                      360                      365

att tat gca ggg      1116
Ile Tyr Ala Gly
      370

<210> 58
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

<400> 58
cct caa atc act ctt tgg caa cga ccc cta gtt aca ata aaa ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly
      1                      5                      10                      15

ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
      20                      25                      30

tta gaa gaa atg act ttg cca gga aaa tgg aaa cca aaa atg ata ggg      144
Leu Glu Glu Met Thr Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly
      35                      40                      45

gga att gga ggt ttt atc aaa gta aga car tat gat cag ata ctc ata      192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Leu Ile
      50                      55                      60

gaa att tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca      240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr
      65                      70                      75                      80

cct gtc aac ata att gga aga aat ctg ttg act cag atc ggt tgc act      288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
      85                      90                      95

tta aat ttt ccc att agt cct att gag act gta cca gta aaa tta aag      336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
      100                      105                      110

cca gga atg gat ggc cca aga gtt aar caa tgg cca ttg aca gaa gaa      384
Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu
      115                      120                      125

aaa ata aaa gca tta gta gaa att tgt aca gaa atg gag aag gaa ggg      432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
      130                      135                      140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt      480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
      145                      150                      155                      160

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gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc      528
Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
                                165                                170                                175

aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga      576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
                                180                                185                                190

ata cca cat cca gca ggg tta aaa aag aaa aaa tca gta aca gta ctg      624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu
                                195                                200                                205

gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg      672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg
                                210                                215                                220

aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg      720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly
                                225                                230                                235                                240

att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca      768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
                                245                                250                                255

gca ata ttc caa agt agc atg aca ata atc tta gag cct ttt aga aaa      816
Ala Ile Phe Gln Ser Ser Met Thr Ile Ile Leu Glu Pro Phe Arg Lys
                                260                                265                                270

caa aat cca gac ata gtt atc tat caa tac atg gat gat ttg tat gta      864
Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val
                                275                                280                                285

gga tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg      912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu
                                290                                295                                300

aga cag cat ctg ttg agg tgg gga ttt acc aca cca gac aaa aaa cat      960
Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His
                                305                                310                                315                                320

cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cca gat     1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
                                325                                330                                335

aaa tgg aca gta cag cct ata aag ctg cca gac aaa gac agc tgg act     1056
Lys Trp Thr Val Gln Pro Ile Lys Leu Pro Asp Lys Asp Ser Trp Thr
                                340                                345                                350

gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag     1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
                                355                                360                                365

att tat gca gga
Ile Tyr Ala Gly
                                370

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<210> 59
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)
<220>

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<221> CDS
 <222> (1)...(297)
 <223> HIV Protease

<221> CDS
 <222> (298)...(1116)
 <223> Portion of HIV Reverse Transcriptase

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<400> 59
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  1                               5                               10                               15

ggg caa cta aaa gaa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
                               20                               25                               30

tta gaa gaa ata aat ttg cca ggg aaa tgg aaa cca maa atg ata ggg      144
Leu Glu Glu Ile Asn Leu Pro Gly Lys Trp Lys Pro Xaa Met Ile Gly
                               35                               40                               45

gga att gga ggt ttt att aaa gta aga cag tat gat caa ata gcc ata      192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Ala Ile
                               50                               55                               60

gaa att tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca      240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr
  65                               70                               75                               80

cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act      288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
                               85                               90                               95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag      336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
                               100                              105                              110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa      384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
                               115                              120                              125

aaa ata aaa gca tta rta gaa atc tgt aca gaa atg gaa aag gaa ggg      432
Lys Ile Lys Ala Leu Xaa Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
                               130                              135                              140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt      480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
                               145                              150                              155                              160

gcm ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc      528
Xaa Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
                               165                              170                              175

aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtc caa tta gga      576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
                               180                              185                              190

ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta cta      624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu
                               195                              200                              205

gat gtg ggt gat gca tat ttc tca gtt ccc tta gac caa gac ttc agg      672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Gln Asp Phe Arg
                               210                              215                              220

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aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240	720
att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agt agc atg aca agg atc tta gar cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Arg Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gaa ata gtc aty tat cag tac atg gat gat tta tat gta Gln Asn Pro Glu Ile Val Xaa Tyr Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac tta gaa ata ggg cag cat aga aca aaa gta gag gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Val Glu Glu Leu 290 295 300	912
aga caa cat ctg ttg agr tgg ggg ttt tmc acg cca gac aaa aag cat Arg Gln His Leu Leu Xaa Trp Gly Phe Xaa Thr Pro Asp Lys Lys His 305 310 315 320	960
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta cag act ata gaa ctg cca gaa aaa gat agc tgg act Lys Trp Thr Val Gln Thr Ile Glu Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056
gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
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ggg caa cta aaa gaa gct cta tta gay aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30	96

tta gaa gaa atg aat ttg cca ggr aga tgg aaa cca aaa atg ata ggg Leu Glu Glu Met Asn Leu Pro Xaa Arg Trp Lys Pro Lys Met Ile Gly	144
35 40 45	
gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata cct rta Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Xaa	192
50 55 60	
gaa att tgt gga cat aaa gct ata ggt aca gta tta ata gga cct aca Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Ile Gly Pro Thr	240
65 70 75 80	
cct gtc aac ata att gga aga aat ctg atg act cag ctt ggc tgc act Pro Val Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Leu Gly Cys Thr	288
85 90 95	
tta aat ttt cct att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys	336
100 105 110	
cca gga atg gat ggc cca aga gtt aaa caa tgg cca ttg aca gaa gag Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu	384
115 120 125	
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa gga Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly	432
130 135 140	
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe	480
145 150 155 160	
gcc ata aag aaa aaa gac agt aat aga tgg aga aaa tta gtg gat ttc Ala Ile Lys Lys Lys Asp Ser Asn Arg Trp Arg Lys Leu Val Asp Phe	528
165 170 175	
aga gaa ctt aat aar aga act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly	576
180 185 190	
ata cca cat cct gca ggg tta raa aag aac aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Xaa Lys Asn Lys Ser Val Thr Val Leu	624
195 200 205	
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gaa ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Glu Phe Arg	672
210 215 220	
aag tat act gca ttt acc ata cct agt acc aat aat gag aca ccm ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Xaa Gly	720
225 230 235 240	
gtt aga tat cag tat aat gta ctt ccc cag gga tgg aaa gga tca cca Val Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro	768
245 250 255	
gca tat tty caa tgt agy atg aca aaa atc tta aag cct ttc agg aaa Ala Tyr Phe Gln Cys Xaa Met Thr Lys Ile Leu Lys Pro Phe Arg Lys	816
260 265 270	
caa aat cca cac ata gtt att ttt caa tat gtg gat gac ttg tat gta Gln Asn Pro His Ile Val Ile Phe Gln Tyr Val Asp Asp Leu Tyr Val	864
275 280 285	

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gca tct gac tta gaa ata gag cag cat aga aca aaa ata gag gaa ctg      912
Ala Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Glu Glu Leu
290                               295                               300

aga caa cat ttg ttg agg tgg gga ctc acc aca cca gac aaa aaa cat      960
Arg Gln His Leu Leu Arg Trp Gly Leu Thr Thr Pro Asp Lys Lys His
305                               310                               315                               320

caa aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat      1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
                               325                               330                               335

aaa tgg aca gta cag ccc ata acg ctg cca gaa aaa gac agc tgg act      1056
Lys Trp Thr Val Gln Pro Ile Thr Leu Pro Glu Lys Asp Ser Trp Thr
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gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag      1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
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att tat gca ggg
Ile Tyr Ala Gly
370

<210> 61
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
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<400> 61
cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata aaa gat agg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Asp Arg
1                               5                               10                               15

ggg gca agt aaa gaa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Ala Ser Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
                               20                               25                               30

tta gaa gaa ata aat ttg cca ggg rag tgg aaa cca aaa atg ata ggg      144
Leu Glu Glu Ile Asn Leu Pro Gly Xaa Trp Lys Pro Lys Met Ile Gly
                               35                               40                               45

gga att gga ggt ttt atc aaa gta aga cag tmt gat cag ata ccc gta      192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Xaa Asp Gln Ile Pro Val
50                               55                               60

gaa att tgt gga cat aag gct ata ggt aca gta tta gta gga cct aca      240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr
65                               70                               75                               80

cct gtc aac ata att gga aga aat ctg ttg act cag mtt ggt tgc act      288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Xaa Gly Cys Thr
                               85                               90                               95

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tta aat ttt ccc atc agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca tta aca gag gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa ggg Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly 130 135 140	432
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca ata ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe 145 150 155 160	480
gcc ata aag aaa aag gac agt act aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528
aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt cag tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat cct gca ggg tta aaa aag aaa aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat gaa agc ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Ser Phe Arg 210 215 220	672
aag tac act gca ttt acc ata ccc agt aca aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly 225 230 235 240	720
rca aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca Xaa Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gaa atg gtt atc tat caa tac atg gat gat ttg tat gta Gln Asn Pro Glu Met Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac tta gag ata gag caa cat aga aca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300	912
aga caa cat ctg ttg agg tgg gga ttt acc aca cca gac aaa aaa cat Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His 305 310 315 320	960
cag aaa gaa cct cca ttt ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
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gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt cag      1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
      355                      360                      365

att tat cca ggg
Ile Tyr Pro Gly
      370

<210> 62
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<212> DNA
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<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

<400> 62
cct caa atc act ctt tgg caa cga ccc atc gtc aca ata aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Ile Gly
      1                      5                      10                      15

ggg cag cta aag gaa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
      20                      25                      30

tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atg ata ggg      144
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
      35                      40                      45

gga att gga ggt ttt atc aaa gta aga caa tat gat cag ata gcc ata      192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Ala Ile
      50                      55                      60

gaa atc tgt gga cat aaa gct ata ggt aca gta tta ata gga cct aca      240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Ile Gly Pro Thr
      65                      70                      75                      80

cct gtc aac ata att gga aga aat ctg atg act cag att ggc tgc act      288
Pro Val Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Ile Gly Cys Thr
      85                      90                      95

tta aat ttt ccc att agt cct att gat act gta cca gta aaa tta aag      336
Leu Asn Phe Pro Ile Ser Pro Ile Asp Thr Val Pro Val Lys Leu Lys
      100                      105                      110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa      384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
      115                      120                      125

aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa ggg      432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
      130                      135                      140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt      480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
      145                      150                      155                      160

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gcc ata aag aaa aag aat agt act aaa tgg aga aaa tta gta gat ttc 528
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 165 170 175

aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga 576
 Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
 180 185 190

ata cca cat ccc gca ggg cta aaa aag aay aaa tca gta aca gta ctg 624
 Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu
 195 200 205

gat gtg ggt gat gca tat ttt tca gtc ccc tta gat gaa gac ttc agg 672
 Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg
 210 215 220

aag tac act gca ttt acc ata cct agt ata aac aat gag aca cca ggg 720
 Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly
 225 230 235 240

rtt aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca 768
 Xaa Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
 245 250 255

tca ata ttc caa tgt agc atg acg aaa atc tta gag cct ttt aga aaa 816
 Ser Ile Phe Gln Cys Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys
 260 265 270

cag aat cca gac ata gtt atc trt caa tac atg gat gat ttg tat gta 864
 Gln Asn Pro Asp Ile Val Ile Xaa Gln Tyr Met Asp Asp Leu Tyr Val
 275 280 285

gca tct gac tta gaa ata gag cag cat aga ata aaa ata gag gaa cta 912
 Ala Ser Asp Leu Glu Ile Glu Gln His Arg Ile Lys Ile Glu Glu Leu
 290 295 300

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 Arg Gln His Leu Leu Lys Trp Gly Phe Tyr Thr Pro Asp Lys Lys Xaa
 305 310 315 320

cag aaa gaa cct cca ttc ctt tgg atg ggt tat gar ctc cat cct gat 1008
 Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
 325 330 335

aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act 1056
 Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
 340 345 350

gtc aat gac ata cag aag ttr gtg gga aaa ctg aat tgg gca agt cag 1104
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att tac cca ggg
 Ile Tyr Pro Gly 1116
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<213> Human Immunodeficiency Virus (HIV)

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 <222> (1)...(297)
 <223> HIV Protease

<221> CDS
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 <223> Portion of HIV Reverse Transcriptase

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1          5          10          15

gga cag cta acg gaa gct yta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Thr Glu Ala Xaa Leu Asp Thr Gly Ala Asp Asp Thr Val
          20          25          30

tta gaa gaa atg act ttg cca gga aaa tgg aaa cca aaa ata ata ggg      144
Leu Glu Glu Met Thr Leu Pro Gly Lys Trp Lys Pro Lys Ile Ile Gly
          35          40          45

ggr att gga ggt ttt atc aaa gta aga cag tat gat cac gta ctt gta      192
Xaa Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp His Val Leu Val
          50          55          60

gaa atc tgt gga cat aaa gct ata ggt aca gta tta ata gga cct aca      240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Ile Gly Pro Thr
65          70          75          80

cct gtc aac ata att gga aga aat ttg atg act cag ctt ggg ttc act      288
Pro Val Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Leu Gly Phe Thr
          85          90          95

tta aat ttt cca att agt cct att gaa act gta cca gta aaa tta aag      336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
          100          105          110

cca ggg atg gat ggc cca aaa gtt aaa caa tgg cca ttg mca gaa gaa      384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Xaa Glu Glu
          115          120          125

aaa ata aaa gca cta aca gaa att tgt aca gaa ttg gaa aag gaa gga      432
Lys Ile Lys Ala Leu Thr Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly
          130          135          140

aaa att tca aga ata ggg cct gaa aat cca tac aat act cca ata ttt      480
Lys Ile Ser Arg Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe
145          150          155          160

gcc ata aag aag aaa aac ggt ayt agg tgg aga aaa tta gta gat ttc      528
Ala Ile Lys Lys Lys Asn Gly Xaa Arg Trp Arg Lys Leu Val Asp Phe
          165          170          175

aga gag cta aat aag aga act caa gac ttc tgg gaa gtt caa cta gga      576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
          180          185          190

ata cca cat cct gca gga cta aaa aag aac aaa tca gta aca gta ctg      624
Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu
          195          200          205

gat gtg ggt gat gca tat ttt tca gtt ccc tta cat gaa gac ttt aga      672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu His Glu Asp Phe Arg
210          215          220

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aag tat acc gca ttc acc ata cct agt aca aac aat gaa aca cca gga 720
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 Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
 245 250 255
 gca ata ttc caa agt agc atg acc aaa atc tta gaa cct ttt aga aaa 816
 Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys
 260 265 270
 caa aat cca gaa atg gtt atc tat caa tac gtg gat gat ttg tat gta 864
 Gln Asn Pro Glu Met Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val
 275 280 285
 gga tct gac tta gaa ata ggg cag cat aga ata aaa ata gag gaa tta 912
 Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ile Lys Ile Glu Glu Leu
 290 295 300
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 Arg Glu His Leu Leu Lys Trp Gly Phe Phe Thr Pro Asp Glu Lys His
 305 310 315 320
 cag aaa gaa cct cca ttt ctt tgg atg ggt tat gaa ctt cat cct gat 1008
 Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
 325 330 335
 aaa tgg aca gtg cag cct ata aaa ctg cca gaa aaa gaa agc tgg act 1056
 Lys Trp Thr Val Gln Pro Ile Lys Leu Pro Glu Lys Glu Ser Trp Thr
 340 345 350
 gtc aat gat ata cag aag tta gtg gga aaa tta aat tgg gca agc cag 1104
 Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
 355 360 365
 att tat cca gga 1116
 Ile Tyr Pro Gly
 370

<210> 64
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 ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta 96
 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
 20 25 30

tta gaa gaa atg aat tta cca gga aaa tgg aaa cca aaa atr ata ggg Leu Glu Glu Met Asn Leu Pro Gly Lys Trp Lys Pro Lys Xaa Ile Gly	144
35 40 45	
gga att gga ggy ttt rtc aaa gta aga cag tat gat cag ata syc ata Gly Ile Gly Xaa Phe Xaa Lys Val Arg Gln Tyr Asp Gln Ile Xaa Ile	192
50 55 60	
gaa atc tgc gga cat aaa gct ata ggt aca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr	240
65 70 75 80	
cct gyc aac ata att gga aga aat ctg ttg act cag ctt ggg tgc act Pro Xaa Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr	288
85 90 95	
tta aat ttt ccc att agt cct att gaa act gta cca gta caa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Gln Leu Lys	336
100 105 110	
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca tta aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu	384
115 120 125	
aag ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa ggg Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly	432
130 135 140	
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe	480
145 150 155 160	
gct ata aag aaa aag gac agt gct aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asp Ser Ala Lys Trp Arg Lys Leu Val Asp Phe	528
165 170 175	
agg gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta ggg Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly	576
180 185 190	
ata cck cat ccc gca ggg ttr aaa aag aaa aaa tca gta aca gta cta Ile Xaa His Pro Ala Gly Xaa Lys Lys Lys Ser Val Thr Val Leu	624
195 200 205	
gat gta ggt gat gca tat ttt tca gtt ccc tta gat caa aac ttc aga Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Gln Asn Phe Arg	672
210 215 220	
aag tat act gca ttc acc ata cct agt ata aac aat gag ayg cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Xaa Pro Gly	720
225 230 235 240	
att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro	768
245 250 255	
gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys	816
260 265 270	
caa aat cca gar ata rtt atc tat caa tac gtg gat gat ttg tat gta Gln Asn Pro Glu Ile Xaa Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val	864
275 280 285	

gga tct gac ttr gaa ata ggg cag cat aga aca aaa ata gag gaa ctg	912
Gly Ser Asp Xaa Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu	
290 295 300	
aga caa cat ytg ttg aag tgg gga ttt acc aca cca gac aag aag cat	960
Arg Gln His Xaa Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His	
305 310 315 320	
cag aaa gaa cct cca ttc ctt tgg atg ggg tat gaa ctc cat cct gat	1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp	
325 330 335	
aaa tgg aca gta cag cct ata atg ctg cca gaa aaa gac agc tgg act	1056
Lys Trp Thr Val Gln Pro Ile Met Leu Pro Glu Lys Asp Ser Trp Thr	
340 345 350	
gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag	1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln	
355 360 365	
att tat gca gga	1116
Ile Tyr Ala Gly	
370	

<210> 65
 <211> 1116
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)

<220>
 <221> CDS
 <222> (1)...(297)
 <223> HIV Protease
 <221> CDS
 <222> (298)...(1116)
 <223> Portion of HIV Reverse Transcriptase

<400> 65	
cct cag atc act ctt tgg caa cga ccc atc gtc aca ata aag ata ggg	48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Ile Gly	
1 5 10 15	
ggg cag cta aag gaa gct cta tta gat aca gga gca gat gat aca gta	96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val	
20 25 30	
tta gaa gac atc aat ttg cca gga aaa tgg aaa cca aaa atg ata ggg	144
Leu Glu Asp Ile Asn Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly	
35 40 45	
gga att gga ggt ttt gtc aaa gta aga gag tat gat cag gta ccc ata	192
Gly Ile Gly Gly Phe Val Lys Val Arg Glu Tyr Asp Gln Val Pro Ile	
50 55 60	
gac atc tgt gga cat aaa gtt ata ggt aca gtg tta gta gga cct aca	240
Asp Ile Cys Gly His Lys Val Ile Gly Thr Val Leu Val Gly Pro Thr	
65 70 75 80	
cct gcc aac ata att gga aga aat ctg ttg act cag ctt ggt tgc act	288
Pro Ala Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr	
85 90 95	

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta gta gar atc tgt aca gaa ttg gaa aag gaa gga Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly 130 135 140	432
aaa att tca aaa att ggg cct gaa aay cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gct ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528
aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta ctr Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Xaa 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gaa ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Glu Phe Arg 210 215 220	672
aag tac act gca ttt acc ata cct agt ata aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240	720
rtt aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca Xaa Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agt agc atg aca aaa att tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gac ata att atc tat caa tac gtg gat gat ttg tat gta Gln Asn Pro Asp Ile Ile Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val 275 280 285	864
gga tct gat ttg gaa ata gag cag cat aga aca aaa ata gag gaa cta Gly Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300	912
aga gaa cat ctg tgg aag tgg gga ttt tac aca cca gac aaa aaa cat Arg Glu His Leu Trp Lys Trp Gly Phe Tyr Thr Pro Asp Lys Lys His 305 310 315 320	960
cag aag gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta cag cct ata aag ytg cca gaa aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Lys Xaa Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056

gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt caa 1104
 Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
 355 360 365

att tat cca ggg 1116
 ile Tyr Pro Gly
 370

<210> 66
 <211> 1116
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)

<220>
 <221> CDS
 <222> (1)...(297)
 <223> HIV Protease

 <221> CDS
 <222> (298)...(1116)
 <223> Portion of HIV Reverse Transcriptase

<400> 66
 cct cag atc act ctt tgg caa cga ccc ctt gtc aca ata aag ata ggg 48
 Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly
 1 5 10 15

ggg caa cta aag gaa gct cta tta gat aca gga gca gat gak rca gta 96
 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Xaa Val
 20 25 30

tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atg ata ggg 144
 Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
 35 40 45

gga att gga ggt ttt atc aaa gta agr car tat gac cag ata ccc ata 192
 Gly Ile Gly Gly Phe Ile Lys Val Xaa Gln Tyr Asp Gln Ile Pro Ile
 50 55 60

gaa atc tgt gga cag aaa gct ata ggt aca gta tta gta gga cct acm 240
 Glu Ile Cys Gly Gln Lys Ala Ile Gly Thr Val Leu Val Gly Pro Xaa
 65 70 75 80

cct gtc aac ata att gga aga aat ctg ttg act caa att ggt tgc act 288
 Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
 85 90 95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
 100 105 110

cca gga atg gat ggc cca aga gtt aaa caa tgg cca ttg aca gaa gaa 384
 Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu
 115 120 125

aaa ata aaa gca tta gca gaa att tgt aca gaa atg gaa aag gaa gga 432
 Lys Ile Lys Ala Leu Ala Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
 130 135 140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt 480
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
 145 150 155 160

gcc ata aag aaa aaa gac agt aat ara tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asp Ser Asn Xaa Trp Arg Lys Leu Val Asp Phe 165 170 175	528
agg gaa ctc aat aag aga act caa gac ttc tgg gaa gtt caa tta ggc Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat ccc gca ggg tta aaa aag aam aaa tca gta aca rta ctr Ile Pro His Pro Ala Gly Leu Lys Lys Xaa Lys Ser Val Thr Xaa Xaa 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg 210 215 220	672
aar tat act gca ttt acc ata cct agt aca wac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Xaa Asn Glu Thr Pro Gly 225 230 235 240	720
att aga tat cag krc aat gtg yyt cca cag gga tgg aaa gga tcm cca Ile Arg Tyr Gln Xaa Asn Val Xaa Pro Gln Gly Trp Lys Gly Xaa Pro 245 250 255	768
gca ata ttc mam agt agc ayg aca aaa att tta gag cct ttt aga aaa Ala Ile Phe Xaa Ser Ser Xaa Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gac ata gtt atc tgt caa tac gtg gat gat ttg tat gta Gln Asn Pro Asp Ile Val Ile Cys Gln Tyr Val Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ttg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300	912
agg caa cat ttg ttg agg tgg ggr ttt acc aca cca gac ara aaa cat Arg Gln His Leu Leu Arg Trp Xaa Phe Thr Thr Pro Asp Xaa Lys His 305 310 315 320	960
cag aaa gag cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta cag cct ata aaa ctg cca gaa aaa gay agc tgg act Lys Trp Thr Val Gln Pro Ile Lys Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056
gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
att tat gca ggg Ile Tyr Ala Gly 370	1116

<210> 67
 <211> 1119
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)
 <220>

<221> CDS
 <222> (1)...(297)
 <223> HIV Protease

<221> CDS
 <222> (298)...(1119)
 <223> Portion of HIV Reverse Transcriptase

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<400> 67
cct caa atc act ctt tgg caa cga cca ata gtc aca ata aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Ile Gly
  1             5             10             15

ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
             20             25             30

cta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atg ata ggg      144
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
             35             40             45

gga att gga ggt ttt aty aaa gta aga cag tat gat cag ata tcc ata      192
Gly Ile Gly Gly Phe Xaa Lys Val Arg Gln Tyr Asp Gln Ile Ser Ile
  50             55             60

gaa atc tgt ggg cat aaa gtt aca ggt aca gtg tta ata gga cct aca      240
Glu Ile Cys Gly His Lys Val Thr Gly Thr Val Leu Ile Gly Pro Thr
  65             70             75

cct gtc aac ata att gga aga aat ctg ttg act cag ctt ggt tgc act      288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr
             85             90             95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag      336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
             100            105            110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa      384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
             115            120            125

aaa ata aaa gca ttg gta gaa att tgt gca gaa atg gaa aag gaa ggg      432
Lys Ile Lys Ala Leu Val Glu Ile Cys Ala Glu Met Glu Lys Glu Gly
             130            135            140

caa att tca aaa att gag cct gaa aat cca tac aat aat cca gta ttt      480
Gln Ile Ser Lys Ile Glu Pro Glu Asn Pro Tyr Asn Asn Pro Val Phe
             145            150            155            160

gtc ata aag aaa aaa gac ggt act aac tgg aga aaa tta ata gat ytc      528
Val Ile Lys Lys Lys Asp Gly Thr Asn Trp Arg Lys Leu Ile Asp Xaa
             165            170            175

aga gaa ctt aat aag aga act caa gat ttc tgg gaa att caa tta gga      576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Ile Gln Leu Gly
             180            185            190

ata cca cat ccc gca ggg tta aaa aag aat aaa tca gta aca gta ctg      624
Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu
             195            200            205

gat gtg ggt gat gca ttt tat tca gtt ccc tta gat gag aac ttc agg      672
Asp Val Gly Asp Ala Phe Tyr Ser Val Pro Leu Asp Glu Asn Phe Arg
             210            215            220

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aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg      720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly
225                               230                               235                               240

att aga tat cag tac aat gtg ctt cca atg gga tgg aaa gga tca cca      768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Met Gly Trp Lys Gly Ser Pro
                               245                               250                               255

gca ata ttc caa agt agc atg aca aaa att tta gag cct ttt aga aaa      816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys
                               260                               265                               270

aac aat cca gac ata gtc atc tat caa tac atg gat gat ttg tat gta      864
Asn Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val
                               275                               280                               285

gca tct gat tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg      912
Ala Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu
                               290                               295                               300

aga gaa cat cta ttr aag tgg gga ttt acc aca cca gac aar aar yat      960
Arg Glu His Leu Xaa Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys Xaa
305                               310                               315                               320

cag aaa gaa cct cca ytc ctt tgg atg ggt tat gaa ctc cat cct gat     1008
Gln Lys Glu Pro Pro Xaa Leu Trp Met Gly Tyr Glu Leu His Pro Asp
                               325                               330                               335

aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act     1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
                               340                               345                               350

gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag     1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
                               355                               360                               365

att tat cca ggg att
Ile Tyr Pro Gly Ile
                               370

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<210> 68
<211> 1119
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

```

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<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

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```

<221> CDS
<222> (298)...(1119)
<223> Portion of HIV Reverse Transcriptase

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<400> 68
cct caa atc act ctt tgg caa cga ccc ctc gtc aca ata aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly
1                               5                               10                               15

gga caa cta aaa gaa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
                               20                               25                               30

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tta gaa gaa atg aat ttg cca ggg aaa tgg aaa cca aaa atg ata ggg Leu Glu Glu Met Asn Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly 35 40 45	144
gga atc gga gga ttt atc aaa gta aga cag tat gag cag ata cac ata Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Glu Gln Ile His Ile 50 55 60	192
gaa atc tgt ggg cat aaa gct ata ggt aca gtr tta ata gga ccc aca Glu Ile Cys Gly His Lys Ala Ile Gly Thr Xaa Leu Ile Gly Pro Thr 65 70 75 80	240
cct gtc aac ata att gga aga aat ctg ttg act cag att ggc tgc act Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr 85 90 95	288
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gag Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa gga Lys Ile Lys Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly 130 135 140	432
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gtt ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528
aga gaa ctt aat aaa aga act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat cct gca ggg ttg aag aag aaa aaa tca gta aca gta cta Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa aac ttt agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asn Phe Arg 210 215 220	672
aag tat act gca ttt acc ata cct agt ata aat aat gaa aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240	720
att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa gct agc atg aca aaa atc tta gag cct ttt aga aaa Ala Ile Phe Gln Ala Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gac atg rtt att tat caa tac atg gat gat ttg tat gta Gln Asn Pro Asp Met Xaa Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864


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ggc tct gac tta gaa ata gga cag cat aga aca aaa ata gaa gaa ctg      912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu
290                               295                               300

aga caa cat ctg ttg agg tgg ggg ttt acc aca cca gac aaa aaa cat      960
Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His
305                               310                               315                               320

cag aaa gaa cct cca ttc ctc tgg atg ggt tat gaa ctc cat cct gat      1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
                               325                               330                               335

aaa tgg aca gta cag cct ata gtg ctg cca gaa aag gac agc tgg act      1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
                               340                               345                               350

gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gcg agt cag      1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
                               355                               360                               365

att tat cca ggg att
Ile Tyr Pro Gly Ile
370

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<210> 69
<211> 1119
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

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<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1119)
<223> Portion of HIV Reverse Transcriptase

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<400> 69
cct cag atc act ctt tgg caa cga ccc cty gtc aca ata aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Xaa Val Thr Ile Lys Ile Gly
1                               5                               10                               15

ggg caa yta aag gaa gct mta tta gay aca gga gca gat gat aca gtg      96
Gly Gln Xaa Lys Glu Ala Xaa Leu Asp Thr Gly Ala Asp Asp Thr Val
                               20                               25                               30

tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa ata ata ggg      144
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Ile Ile Gly
                               35                               40                               45

gga att gga ggt ttt atc aaa gta aga gag tat gag cag ata caa gta      192
Gly Ile Gly Gly Phe Ile Lys Val Arg Glu Tyr Glu Gln Ile Gln Val
50                               55                               60

gaa atc tgt gga cat aag gct ata rgt aca gta tta ata gga cct aca      240
Glu Ile Cys Gly His Lys Ala Ile Xaa Thr Val Leu Ile Gly Pro Thr
65                               70                               75                               80

cct gtc aac ata att gga aga aat cta atg act cag att ggt tgc act      288
Pro Val Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Ile Gly Cys Thr
                               85                               90                               95

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tta aat ttt ccc att agt cct att gag act gta ccg gta aaa tta aag	336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys	
100 105 110	
cca gga atg gat ggt cca aga gtt aaa caa tgg cca ttg aca gaa gaa	384
Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu	
115 120 125	
aaa ata aaa gca tta gta gaa att tgt aca gaa ttg gaa aag gaa gga	432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly	
130 135 140	
aaa att tca aaa att ggg cct gaa aat cca tac aat acy ccr gta ttt	480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Xaa Xaa Val Phe	
145 150 155 160	
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc	528
Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe	
165 170 175	
aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga	576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly	
180 185 190	
ata ccg cat ccc gca ggg tta aag aag aaa aaa tca gta aca gta ctr	624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Xaa	
195 200 205	
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg	672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg	
210 215 220	
aag tac act gca ttt acc ata cct agt ata aac aat gag aca cca gga	720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly	
225 230 235 240	
att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca	768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro	
245 250 255	
gca ata ttc caa agt agc atg aca aaa atc tta gaa cct ttt aga aaa	816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys	
260 265 270	
caa aat cca gac ata gtt atc tat car tac atg gat gac ttg tat gta	864
Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val	
275 280 285	
gga tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa cta	912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu	
290 295 300	
aga caa cat ctg tkg agg tgg gga ttt tac aca cca gac aaa aaa cat	960
Arg Gln His Leu Xaa Arg Trp Gly Phe Tyr Thr Pro Asp Lys Lys His	
305 310 315 320	
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cac cct gat	1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp	
325 330 335	
aaa tgg aca gta cag cct ata gtg ctr cca gaa aaa gac agc tgg act	1056
Lys Trp Thr Val Gln Pro Ile Val Xaa Pro Glu Lys Asp Ser Trp Thr	
340 345 350	

gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gcg agt cag 1104
 Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
 355 360 365

att tat tca ggg att 1119
 Ile Tyr Ser Gly Ile
 370

<210> 70
 <211> 1119
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)

<220>
 <221> CDS
 <222> (1)...(297)
 <223> HIV Protease

<221> CDS
 <222> (298)...(1119)
 <223> Portion of HIV Reverse Transcriptase

<400> 70
 cct caa atc act ctt tgg caa cga ccc cty gtc kca ata aag gta ggr 48
 Pro Gln Ile Thr Leu Trp Gln Arg Pro Xaa Val Xaa Ile Lys Val Xaa
 1 5 10 15

ggg caa mta aag gaa gct yta tta gat aca gga gca gat gat aca gta 96
 Gly Gln Xaa Lys Glu Ala Xaa Leu Asp Thr Gly Ala Asp Thr Val
 20 25 30

tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atg ata ggg 144
 Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
 35 40 45

gga att gga ggt ttt atc aaa gta aaa cag tat gat cag gta arc ata 192
 Gly Ile Gly Gly Phe Ile Lys Val Lys Gln Tyr Asp Gln Val Xaa Ile
 50 55 60

gaa atc tgt gga cat aaa gct ata ggt aca gta tta ata gga cct aca 240
 Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Ile Gly Pro Thr
 65 70 75 80

cct gtc aac ata att gga aga aay ctg ttg aca cag att ggt tgy act 288
 Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
 85 90 95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
 100 105 110

cca gga atg gat ggc cca ara gty aaa caa tgg cca ttg aca gaa gaa 384
 Pro Gly Met Asp Gly Pro Xaa Xaa Lys Gln Trp Pro Leu Thr Glu Glu
 115 120 125

aaa ata aar gca tta atg gaa att tgt gca gay atg gaa aag gaa ggr 432
 Lys Ile Lys Ala Leu Met Glu Ile Cys Ala Asp Met Glu Lys Glu Xaa
 130 135 140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt 480
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
 145 150 155 160

gcy ata aag aaa aaa gac agc act aaa tgg aga aaa tta gta gat ttc Xaa Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528
aga gaa ctt aat aag aaa act caa gac ttt tgg gaa gtc caa tta gga Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat ccy gca ggg tta aaa aag aac aaa tca gta aca gta ttg Ile Pro His Xaa Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtt ccy tta gat aaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Xaa Leu Asp Lys Asp Phe Arg 210 215 220	672
aaa tay act gca ttt acm ata cct agt ata aat aat gca aca cca ggg Lys Tyr Thr Ala Phe Xaa Ile Pro Ser Ile Asn Asn Ala Thr Pro Gly 225 230 235 240	720
att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga rar Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Xaa 260 265 270	816
cag aat cca gac ata gtt atc tat caa tac atg gat gay ttg tat gta Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac tta gaa mta ggg cag cat aga rca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Xaa Gly Gln His Arg Xaa Lys Ile Glu Glu Leu 290 295 300	912
aga caa cat ctg tta agg tgg ggg ttt acc acw cca gac aag aaa cat Arg Gln His Leu Leu Arg Trp Gly Phe Thr Xaa Pro Asp Lys Lys His 305 310 315 320	960
cag aaa gaa ccc cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta car ccc ata gtg ttg cca gaa aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056
gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
att tay gsa ggg att Ile Tyr Xaa Gly Ile 370	1119

<210> 71

<211> 1119

<212> DNA

<213> Human Immunodeficiency Virus (HIV)

<220>

<221> CDS
 <222> (1)...(297)
 <223> HIV Protease

<221> CDS
 <222> (298)...(1119)
 <223> Portion of HIV Reverse Transcriptase

```

<400> 71
cct caa atc act ctt tgg caa cga ccc atc gtc tca ata aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Ser Ile Lys Ile Gly
  1             5             10             15

ggg gca aat aaa gaa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Ala Asn Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
             20             25             30

tta gaa gaa atg aat ttg cca gga aga tgg aag cca aaa atg ata gtg      144
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Val
             35             40             45

gga att gga ggt ttt agc aaa gta aga caa tat gat cag ata ccc ata      192
Gly Ile Gly Gly Phe Ser Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile
  50             55             60

gaa atc tgc gga cgt aaa gtt gta ggt tca gta tta ata gga cct aca      240
Glu Ile Cys Gly Arg Lys Val Val Gly Ser Val Leu Ile Gly Pro Thr
  65             70             75             80

cct gcc aac ata att gga aga aat ctg ttg act cag ctt ggc tgt act      288
Pro Ala Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr
             85             90             95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag      336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
             100            105            110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca aaa gag      384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Lys Glu
             115            120            125

aaa ata aaa gca tta ata gaa att tgt aca gaa ttg gaa gaa gaa gga      432
Lys Ile Lys Ala Leu Ile Glu Ile Cys Thr Glu Leu Glu Glu Xaa Gly
             130            135            140

aaa att aca aaa att ggg cct gaa aat ccg tac aat act cca ata ttt      480
Lys Ile Thr Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe
             145            150            155            160

gcc ata aag aaa aar aac agt act aaa tgg aga aaa tta gta gac ttc      528
Ala Ile Lys Lys Lys Asn Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
             165            170            175

agg gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga      576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
             180            185            190

ata cca cat cct gca ggg tta aaa aag aaa aaa tca gta aca gta ctg      624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu
             195            200            205

gat gtg ggt gat gca tat ttt tca att ccc tta gat aaa gac ttc agg      672
Asp Val Gly Asp Ala Tyr Phe Ser Ile Pro Leu Asp Lys Asp Phe Arg
             210            215            220

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aar tat act gca ttt acc ata cct agt acg aat aat gag aca cca ggg	720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly	
225 230 235 240	
att aga tat cag tat aat gtg ctt cca cag gga tgg aaa gga tca cca	768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro	
245 250 255	
gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa	816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys	
260 265 270	
caa aat ccc gac ata gtt atc tat caa tac gtg gat gat ttg ctt gta	864
Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Leu Val	
275 280 285	
gga tct gac tta gaa ata gag cag cat aga aca aaa ata gag gag cta	912
Gly Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Glu Glu Leu	
290 295 300	
aga caa cat ctg tgg aag tgg gga ttt tac aca cca gac aaa aaa cat	960
Arg Gln His Leu Trp Lys Trp Gly Phe Tyr Thr Pro Asp Lys Lys His	
305 310 315 320	
cag aaa gaa ccc cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat	1008
Gln Lys Glu Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp	
325 330 335	
aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act	1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr	
340 345 350	
gtc aat gac ata caa aag tta gtg gga aaa tta aat tgg gcw agt cag	1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Xaa Ser Gln	
355 360 365	
att tat cca ggg att	1119
Ile Tyr Pro Gly Ile	
370	

<210> 72

<211> 1119

<212> DNA

<213> Human Immunodeficiency Virus (HIV)

<220>

<221> CDS

<222> (1)...(297)

<223> HIV Protease

<221> CDS

<222> (298)...(1119)

<223> Portion of HIV Reverse Transcriptase

<400> 72

cct cag atc act ctt tgg caa cga ccc cty gtc aca ata aag atc ggg	48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Xaa Val Thr Ile Lys Ile Gly	
1 5 10 15	

ggg caa tta aag gaa gct cta tta gat aca gga gca gat gat aca gta	96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val	
20 25 30	

ata gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atg ata ggg Ile Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly 35 40 45	144
gga att gga ggt ttt rtc aaa gta aga caa tat gat cag gta ccc ata Gly Ile Gly Gly Phe Xaa Lys Val Arg Gln Tyr Asp Gln Val Pro Ile 50 55 60	192
gaa att tgc gga cat aaa gct ata ggt aca gta tta ata gga cct aca Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Ile Gly Pro Thr 65 70 75 80	240
cct gyc aac ata att gga aga aac ctg ttg act caa ctt ggc tgc act Pro Xaa Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr 85 90 95	288
tta aat ttt cca att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta gta gaa att tgt aca gaa ctg gaa aaa gga agg Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Gly Arg 130 135 140	432
aaa aat tac aaa att ggg cct gaa aac cca tac aat act cca gta ttt Lys Asn Tyr Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528
aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat cct gca ggg tta aaa aag aaa aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttc tca gtt ccc tta gat aag gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg 210 215 220	672
aag tat act gca ttt acc ata cct agc ata aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240	720
att aga tat cag tac aat gtg ctc cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gcm ata ttc caa tgt agc atg aca aaa atc tta gag cct ttt aga aaa Xaa Ile Phe Gln Cys Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gaa ata gtt atc tat caa tac atg gat gat ttg tat gta Gln Asn Pro Glu Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864

ggg tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg	912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu	
290 295 300	
aga cga cat ctg ttg aag tgg gga ttt tac aca cca gac aaa aaa cat	960
Arg Arg His Leu Leu Lys Trp Gly Phe Tyr Thr Pro Asp Lys Lys His	
305 310 315 320	
cag aaa gaa ccc cca ttc ctt tgg atg ggt tat gag ctc cat cct gat	1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp	
325 330 335	
aaa tgg aca gta caa cct ata gtg cta cca gag aaa gac agc tgg act	1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr	
340 345 350	
gtc aat gac ata cag aag tta gtg gga aag tta aat tgg gca agt cag	1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln	
355 360 365	
ata tac gca ggg att	1119
Ile Tyr Ala Gly Ile	
370	

<210> 73

<211> 1119

<212> DNA

<213> Human Immunodeficiency Virus (HIV)

<220>

<221> CDS

<222> (1)...(297)

<223> HIV Protease

<221> CDS

<222> (298)...(1119)

<223> Portion of HIV Reverse Transcriptase

<400> 73

cct caa atc act ctt tgg caa cga ccc ttc gtc aca gta aag ata ggg	48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Phe Val Thr Val Lys Ile Gly	
1 5 10 15	
ggg cag cta aag gaa gct cta tta gat aca gga gca gat aat aca gta	96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asn Thr Val	
20 25 30	
tta gaa gaa atg aat tta ccg gga aga tgg aaa cca aaa atg ata ggg	144
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly	
35 40 45	
gga att gga ggt ttt atc aaa gta aga cag tat gat cag rta ccc ata	192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Xaa Pro Ile	
50 55 60	
gaa atc tgt gga cac aaa gct ata ggt aca gta tta ata gga cct aca	240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Ile Gly Pro Thr	
65 70 75 80	
cct gtc aac ata att gga aga gat ctg ttg act cag ctt ggt tgc act	288
Pro Val Asn Ile Ile Gly Arg Asp Leu Leu Thr Gln Leu Gly Cys Thr	
85 90 95	

tta	aat	ttt	ccc	att	agt	cct	att	gat	act	gta	cca	gta	aaa	tta	aaa	336
Leu	Asn	Phe	Pro	Ile	Ser	Pro	Ile	Asp	Thr	Val	Pro	Val	Lys	Leu	Lys	
			100					105					110			
cca	gga	atg	gat	ggc	cca	aaa	gtt	aaa	caa	tgg	cca	ttg	aca	gaa	gaa	384
Pro	Gly	Met	Asp	Gly	Pro	Lys	Val	Lys	Gln	Trp	Pro	Leu	Thr	Glu	Glu	
		115					120					125				
aaa	ata	aaa	gca	tta	gta	gaa	att	tgt	aca	gaa	ctg	gaa	aag	gaa	ggg	432
Lys	Ile	Lys	Ala	Leu	Val	Glu	Ile	Cys	Thr	Glu	Leu	Glu	Lys	Glu	Gly	
	130					135					140					
aag	att	tca	aaa	att	ggg	cct	gaa	aat	cca	tac	aat	acc	cca	gta	ttt	480
Lys	Ile	Ser	Lys	Ile	Gly	Pro	Glu	Asn	Pro	Tyr	Asn	Thr	Pro	Val	Phe	
145					150					155					160	
gct	ata	aag	aaa	aaa	gac	agt	act	aaa	tgg	aga	aag	tta	gta	gat	ttc	528
Ala	Ile	Lys	Lys	Lys	Asp	Ser	Thr	Lys	Trp	Arg	Lys	Leu	Val	Asp	Phe	
				165					170					175		
aga	gaa	ctt	aat	aag	aga	act	caa	gac	ttc	tgg	gaa	gtt	caa	tta	gga	576
Arg	Glu	Leu	Asn	Lys	Arg	Thr	Gln	Asp	Phe	Trp	Glu	Val	Gln	Leu	Gly	
			180					185					190			
ata	cca	cat	ccc	gcg	ggg	tta	aaa	aag	aac	aaa	tca	gta	aca	gta	ctg	624
Ile	Pro	His	Pro	Ala	Gly	Leu	Lys	Lys	Asn	Lys	Ser	Val	Thr	Val	Leu	
		195					200					205				
gat	gtg	ggt	gat	gca	tat	ttt	tca	gtt	ccc	tta	gat	aaa	gac	ttc	agg	672
Asp	Val	Gly	Asp	Ala	Tyr	Phe	Ser	Val	Pro	Leu	Asp	Lys	Asp	Phe	Arg	
	210					215					220					
aag	tat	act	gca	ttt	acc	ata	cct	agt	ata	aac	aat	gag	aca	cca	ggg	720
Lys	Tyr	Thr	Ala	Phe	Thr	Ile	Pro	Ser	Ile	Asn	Asn	Glu	Thr	Pro	Gly	
225					230					235					240	
att	aga	tat	cag	tac	aat	gtg	ctt	ccc	cag	gga	tgg	aaa	gga	tca	cca	768
Ile	Arg	Tyr	Gln	Tyr	Asn	Val	Leu	Pro	Gln	Gly	Trp	Lys	Gly	Ser	Pro	
			245						250					255		
gca	ata	ttc	caa	agt	agc	atg	aca	aaa	att	tta	gag	cct	ttt	aga	aaa	816
Ala	Ile	Phe	Gln	Ser	Ser	Met	Thr	Lys	Ile	Leu	Glu	Pro	Phe	Arg	Lys	
			260					265					270			
cag	aat	cca	gac	ata	gtt	atc	tac	caa	tac	gtg	gat	gac	ttg	tat	gta	864
Gln	Asn	Pro	Asp	Ile	Val	Ile	Tyr	Gln	Tyr	Val	Asp	Asp	Leu	Tyr	Val	
		275					280					285				
gga	tct	gac	tta	gaa	ata	ggg	cag	cat	aga	gca	aaa	ata	gat	gag	ctg	912
Gly	Ser	Asp	Leu	Glu	Ile	Gly	Gln	His	Arg	Ala	Lys	Ile	Asp	Glu	Leu	
	290					295					300					
agg	caa	cat	ctg	ttg	aag	tgg	gga	ttt	tac	aca	cca	gac	aaa	aag	cat	960
Arg	Gln	His	Leu	Leu	Lys	Trp	Gly	Phe	Tyr	Thr	Pro	Asp	Lys	Lys	His	
305					310					315					320	
cag	aaa	gaa	cca	cca	ttc	ctt	tgg	atg	ggk	tat	gaa	ctc	cat	cct	gat	1008
Gln	Lys	Glu	Pro	Pro	Phe	Leu	Trp	Met	Xaa	Tyr	Glu	Leu	His	Pro	Asp	
				325					330					335		
aaa	tgg	aca	gta	cag	cct	ata	gtg	ctg	cca	gaa	aar	gac	agc	tgg	act	1056
Lys	Trp	Thr	Val	Gln	Pro	Ile	Val	Leu	Pro	Glu	Lys	Asp	Ser	Trp	Thr	
			340					345					350			

gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag 1104
 Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
 355 360 365

att tac cca ggg att 1119
 Ile Tyr Pro Gly Ile
 370

<210> 74
 <211> 1116
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)

<220>
 <221> CDS
 <222> (1)...(297)
 <223> HIV Protease

<221> CDS
 <222> (298)...(1116)
 <223> Portion of HIV Reverse Transcriptase

<400> 74
 cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata aag gtc ggg 48
 Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Val Gly
 1 5 10 15

ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta 96
 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
 20 25 30

tta gag gaa cta aat ttg cca gga aga tgg aaa cca aaa atg ata ggg 144
 Leu Glu Glu Leu Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
 35 40 45

gga att gga ggt ttt atc aaa gta aaa cag tat gat cag ata ccc ata 192
 Gly Ile Gly Gly Phe Ile Lys Val Lys Gln Tyr Asp Gln Ile Pro Ile
 50 55 60

gaa ata tgt gga cat aaa gct att ggt aca gta tta gta gga cct aca 240
 Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr
 65 70 75 80

cct gtc aac ata att gga aga aac ttg ttg act cag ctt ggt tgc act 288
 Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr
 85 90 95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
 100 105 110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
 115 120 125

aaa ata aaa gca tta aca gaa att tgt aca gaa atg gaa aag gaa ggg 432
 Lys Ile Lys Ala Leu Thr Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
 130 135 140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt 480
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
 145 150 155 160

gct ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528
aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat ccc gca ggt tta aaa aag aaa aaa tca gta aca gtc ctg Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gaa ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Glu Phe Arg 210 215 220	672
aag tac act gca ttt acc ata cct agt ata aac aat gag aca cca gga Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240	720
att aga tac cag tac aat gtg ctt ccc cag ggg tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt agg aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gac ata gtt atc tac caa tac atg gat gat ttg tat gta Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300	912
aga cag cat ctg ttg agg tgg gga ttt acc aca cca gac aaa aag cat Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His 305 310 315 320	960
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gag ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta cag cct ata gtg ctg cca gaa aag gat agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056
gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
att tat gca ggg Ile Tyr Ala Gly 370	1116

<210> 75
 <211> 819
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)
 <220>

<221> CDS

<222> (1)...(819)

<223> Portion of HIV Reverse Transcriptase

<400> 75

ccc att agt cct att gam act gta cca gta aaa tta aag cca gga atg	48
Pro Ile Ser Pro Ile Xaa Thr Val Pro Val Lys Leu Lys Pro Gly Met	
1 5 10 15	
gat ggc cca aaa gtt aaa caa tgg cca tta aca gag gaa aaa ata aaa	96
Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu Lys Ile Lys	
20 25 30	
gca ttg gta gaa att tgt aca gaa atg gaa aag gaa gga aaa att tca	144
Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly Lys Ile Ser	
35 40 45	
aaa att ggg cct gaa aat cca tac aat act cca gta ttt gcc ata aag	192
Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe Ala Ile Lys	
50 55 60	
aaa aag gac agt act aaa tgg aga aaa tta gta gat ttc aga gaa ctt	240
Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe Arg Glu Leu	
65 70 75 80	
aat aar aga act caa gat ttc tgg gaa gtt caa tta gga ata cca cat	288
Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly Ile Pro His	
85 90 95	
ccc tca ggg tta aaa aag aay aaa tca gta aca gta ttg gat gtg ggt	336
Pro Ser Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu Asp Val Gly	
100 105 110	
gat gca tat ttt tca gtt ccy tta gat aaa gac ttc agg aag tat act	384
Asp Ala Tyr Phe Ser Val Xaa Leu Asp Lys Asp Phe Arg Lys Tyr Thr	
115 120 125	
gca ttt acc ata cct agt ata aac aat gag aca cca ggg att agr tat	432
Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly Ile Xaa Tyr	
130 135 140	
cag tac aat gtg ctt cca caa gga tgg aaa gga tca cca gca ata ttc	480
Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro Ala Ile Phe	
145 150 155 160	
caa agt agc atg aca aaa atc tta gag cct ttt aga aaa cat aat cca	528
Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys His Asn Pro	
165 170 175	
gac ata gtt atc tat caa tac gtg gat gat ttg tat gta gga tct gac	576
Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val Gly Ser Asp	
180 185 190	
tta gaa ata gag gag cat aga aca aaa ata gag gaa ctg agr vrg cat	624
Leu Glu Ile Glu Glu His Arg Thr Lys Ile Glu Glu Leu Xaa Xaa His	
195 200 205	
ctg tta aag tgg gga ttt acy aca cca gac aaa aag cat cag aaa gaa	672
Leu Leu Lys Trp Gly Phe Xaa Thr Pro Asp Lys Lys His Gln Lys Glu	
210 215 220	
cct cca ttt ctt tgg atg ggt tat gaa ctc cat cct gat aaa tgg aca	720
Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp Lys Trp Thr	
225 230 235 240	

gta cag cct ata aag ctg cca gaa aaa gac agc tgg act gtc aat gac 768
Val Gln Pro Ile Lys Leu Pro Glu Lys Asp Ser Trp Thr Val Asn Asp
245 250 255

ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag att tat gca 816
Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln Ile Tyr Ala
260 265 270

ggg 819
Gly

<210> 76

<211> 819

<212> DNA

<213> Human Immunodeficiency Virus (HIV)

<220>

<221> CDS

<222> (1)...(819)

<223> Portion of HIV Reverse Transcriptase

<400> 76

ccc att agt cct att gaa act gta cca gta aaa tta aag cca gga atg 48
Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys Pro Gly Met
1 5 10 15

gat ggc cca aaa gty aaa caa tgg cca tta aca gaa gaa aaa ata aga 96
Asp Gly Pro Lys Xaa Lys Gln Trp Pro Leu Thr Glu Glu Lys Ile Arg
20 25 30

gca tta gta gaa att tgt aca gaa atg gaa aag gaa gga aaa att tca 144
Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly Lys Ile Ser
35 40 45

aaa att ggg cct gaa aat cca tac aat act cca gtg ttt gct ata aag 192
Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe Ala Ile Lys
50 55 60

aaa aaa gac agt act aar tgg aga aaa ttg gta gat ttc aga gaa ctt 240
Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe Arg Glu Leu
65 70 75 80

aat aag aga act caa gac ttc tgg gaa gtt caa tta gga ata cca cat 288
Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly Ile Pro His
85 90 95

ccc tca ggg tta aaa aag aaa aaa tca gta aca gta ctg gat gtg ggt 336
Pro Ser Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu Asp Val Gly
100 105 110

gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg aag tat act 384
Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg Lys Tyr Thr
115 120 125

gca ttt act atn cct agt ata aac aat gag aca cca ggg att agg tat 432
Ala Phe Thr Xaa Pro Ser Ile Asn Asn Glu Thr Pro Gly Ile Arg Tyr
130 135 140

cag tac aat gtg ctt cca caa gga tgg aaa gga tca cca gca ata ttc 480
Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro Ala Ile Phe
145 150 155 160

caa agt agc atg aca aaa atc tta gag cct ttt aga aaa caa aat cca	528
Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys Gln Asn Pro	
165 170 175	
gac ata gtt atc tat caa tac gtg gat gat ttg tat gta gga tct gac	576
Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val Gly Ser Asp	
180 185 190	
cta gaa ata gga cag cat aga aca aaa ata gag gaa ctg aga cag cat	624
Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu Arg Gln His	
195 200 205	
ctg ttg agg tgg gga ttt acc aca cca gac aag aaa cat cag aaa gaa	672
Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His Gln Lys Glu	
210 215 220	
cct ccc ttt ctt tgg atg ggc tat gaa ctc cat cct gat aaa tgg aca	720
Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp Lys Trp Thr	
225 230 235 240	
gta cag cct ata gag ctg cca gac aag gat agc tgg act gtc aat gac	768
Val Gln Pro Ile Glu Leu Pro Asp Lys Asp Ser Trp Thr Val Asn Asp	
245 250 255	
ata cag aag tta gtg gga aaa tta aat tgg gca agt cag ata tat gca	816
Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln Ile Tyr Ala	
260 265 270	
ggg	819
Gly	

<210> 77
 <211> 1116
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)

<220>
 <221> CDS
 <222> (1)...(297)
 <223> HIV Protease

<221> CDS
 <222> (298)...(1116)
 <223> Portion of HIV Reverse Transcriptase

<400> 77	
cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata aag ata ggg	48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly	
1 5 10 15	
ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta	96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val	
20 25 30	
tta gaa gac atg aat ttg cca ggg aga tgg aaa cca aaa atg ata ggg	144
Leu Glu Asp Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly	
35 40 45	
gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata cct ata	192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile	
50 55 60	

gaa atc tgc gga cat aaa gct gta ggt aaa gta tta gta gga cct aca Glu Ile Cys Gly His Lys Ala Val Gly Lys Val Leu Val Gly Pro Thr 65 70 75 80	240
cct gtc aac ata att gga aga aat ctg ttg act caa ctt ggt tgc act Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr 85 90 95	288
tta aat ttt cct att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtt aag caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gag aag gaa ggg Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly 130 135 140	432
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gct ata aag aaa aaa aac agt act aga tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asn Ser Thr Arg Trp Arg Lys Leu Val Asp Phe 165 170 175	528
aga gaa ctt aat aag aga acg caa gac ttc tgg gaa gtt caa nnn nnn Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Xaa Xaa 180 185 190	576
nnn nnn nnn nnn nnn ggg twa aaa aag aaa aaa tca gta aca gta ctg Xaa Xaa Xaa Xaa Gly Xaa Lys Lys Lys Ser Val Thr Val Leu 195 200 205	624
gat gta ggt gat gca tat ttc tca gtt cct cta gat aaa gac ttc aga Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg 210 215 220	672
aag tac act gca ttc acc ata cct agt ata aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240	720
att aga tat cag tac aat gtg ctg cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gac ata gtt atc tat caa tac gtg gat gat ttg tat gtg Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300	912
aga caa cat ttg ttg aag tgg gga ttt acc aca cca gac aaa aaa cat Arg Gln His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His 305 310 315 320	960

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cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat      1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
          325                      330                      335

aaa tgg aca gta cag cct ata gtg ctg cca gaa aag gac agc tgg act      1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
          340                      345                      350

gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agc cag      1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
          355                      360                      365

ata tat gca ggg
Ile Tyr Ala Gly
          370

<210> 78
<211> 1122
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1122)
<223> Portion of HIV Reverse Transcriptase

<400> 78
cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly
  1              5              10              15

ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
          20              25              30

tta gaa gac atg gat ttg cca gga aga tgg aaa cca aaa atg ata ggg      144
Leu Glu Asp Met Asp Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
          35              40              45

gga att gga ggt ttt atc aaa gta aaa cag tat gat cag ata ccc ata      192
Gly Ile Gly Gly Phe Ile Lys Val Lys Gln Tyr Asp Gln Ile Pro Ile
          50              55              60

gaa atc tgt gga cat aaa gtt ata ggt aca gta tta gta gga cct aca      240
Glu Ile Cys Gly His Lys Val Ile Gly Thr Val Leu Val Gly Pro Thr
          65              70              75              80

cct gtc aac ata att gga aga aat ctg ttg act cag ctt ggt tgc act      288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr
          85              90              95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag      336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
          100              105              110

cca gga atg gat ggc cca aga gtt aaa caa tgg cca ttg aca gaa gaa      384
Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu
          115              120              125

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aaa ata aaa gca ttg gta gaa ata tgt aca gaa atg gaa aag gaa ggg Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly 130 135 140	432
aaa att tca aaa att ggg cct gaa aat cca tac aat acr cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Xaa Pro Val Phe 145 150 155 160	480
gcc ata arg aaa aaa gaa agc tct agc tct aaa tgg aga aaa tta gta Ala Ile Xaa Lys Lys Glu Ser Ser Ser Lys Trp Arg Lys Leu Val 165 170 175	528
gat ttc aga gaa ctt aat aar aga act caa gac ttt ttk gaa gtt caa Asp Phe Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Xaa Glu Val Gln 180 185 190	576
tta gga ata cca cat ccc gca ggg tta aag aag aaa aaa tca gya aca Leu Gly Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Xaa Thr 195 200 205	624
rta ttg gat gtg ggt gat gca tat ttt tca gtt ccc tta gat raa gac Xaa Leu Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Xaa Asp 210 215 220	672
ttc agg aag tat act gca ttt acc ata cct agt ata aac aat gag aca Phe Arg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr 225 230 235 240	720
cca ggg att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga Pro Gly Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly 245 250 255	768
tca cca gct ata ttc caa agt agc atg aca aaa atc tta gag cct ttt Ser Pro Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe 260 265 270	816
aga aaa caa aat cca gay ata gtt atc tat caa tac atg gat gat ttg Arg Lys Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu 275 280 285	864
tat gta gga tct gay tta gaa ata gag cag cat aga ata aaa ata gag Tyr Val Gly Ser Asp Leu Glu Ile Glu Gln His Arg Ile Lys Ile Glu 290 295 300	912
gaa ctg aga caa yat ytg tgg arg tgg ggr ttt tac aca cca gac aaa Glu Leu Arg Gln Xaa Xaa Trp Xaa Trp Xaa Phe Tyr Thr Pro Asp Lys 305 310 315 320	960
aaa cat cag aaa gaa cct cca ttc cat tgg atg ggt tat gaa ctc cat Lys His Gln Lys Glu Pro Pro Phe His Trp Met Gly Tyr Glu Leu His 325 330 335	1008
cct gat aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc Pro Asp Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser 340 345 350	1056
tgg act gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca Trp Thr Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala 355 360 365	1104
agt cag att tat gca ggr Ser Gln Ile Tyr Ala Xaa 370	1122

<210> 79
 <211> 1116
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)

<220>
 <221> CDS
 <222> (1)...(297)
 <223> HIV Protease

<221> CDS
 <222> (298)...(1116)
 <223> Portion of HIV Reverse Transcriptase

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<400> 79
cct cag atc act ctt tgg caa cga ccc ctc gtt aca ata aag gta ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Val Gly
   1               5               10               15

ggg caa cta aag gaa gct cta tta gat aca gga gca gac aat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asn Thr Val
               20               25               30

ttc gaa gac ctg gat tta cca gga agg tgg aaa cca aaa atg ata ggg     144
Phe Glu Asp Leu Asp Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
               35               40               45

gga att gga ggt ttt atc aaa gta aaa cag tat gag cag ata ccc ata     192
Gly Ile Gly Gly Phe Ile Lys Val Lys Gln Tyr Glu Gln Ile Pro Ile
   50               55               60

gaa atc tgt ggg cgt aaa gct ata ggt aca gtg tta gta gga cct aca     240
Glu Ile Cys Gly Arg Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr
   65               70               75

cct gtc aac ata att gga aga gat ctg ttg act cag att ggt tgc act     288
Pro Val Asn Ile Ile Gly Arg Asp Leu Leu Thr Gln Ile Gly Cys Thr
               85               90               95

cta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag     336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
               100              105              110

cca gga atg gat ggc cca aga gtt aaa caa tgg cca ttg aca gaa gaa     384
Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu
               115              120              125

aaa ata aaa gca tta ata gaa att tgt gca gaa atg gaa aag gaa ggg     432
Lys Ile Lys Ala Leu Ile Glu Ile Cys Ala Glu Met Glu Lys Glu Gly
               130              135              140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt     480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
               145              150              155

gcc ata aag aaa aag aac agt aat aaa tgg aga aaa tta gta gat ttc     528
Ala Ile Lys Lys Lys Asn Ser Asn Lys Trp Arg Lys Leu Val Asp Phe
               165              170              175

aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga     576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
               180              185              190

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ata cca cat ccc gca ggg tta aaa aag aaa aag tca ata aca gta tta Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Ile Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttc tca gtt ccc tta gat gaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg 210 215 220	672
aag tat act gca ttt acc ata cct agt aca aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly 225 230 235 240	720
att aga tat cag tac aat gtg ctg cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agt agc atg aca aaa att tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gac ata gtt atc tat caa tac atg gat gat ttg tat gta Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864
gga tct gat tta gaa ata gag cag cat aga aca aaa ata gat gaa ctg Gly Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Asp Glu Leu 290 295 300	912
aga caa cat ctg ttg agg tgg gga ctt acc aca cca gac cag aaa cat Arg Gln His Leu Leu Arg Trp Gly Leu Thr Thr Pro Asp Gln Lys His 305 310 315 320	960
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta cag cct ata gtg ctg cca gac aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Asp Lys Asp Ser Trp Thr 340 345 350	1056
gtc aat gac ata cag aag tta gtg ggr aaa ttg aat tgg gca agt caa Val Asn Asp Ile Gln Lys Leu Val Xaa Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
att tac cca ggg Ile Tyr Pro Gly 370	1116

<210> 80
 <211> 1119
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)

<220>
 <221> CDS
 <222> (1)...(297)
 <223> HIV Protease

<221> CDS
 <222> (298)...(1119)
 <223> Portion of HIV Reverse Transcriptase

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<400> 80
cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly
1      5      10      15

ggg cag cta aag gag gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
20      25      30

tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atg ata ggg      144
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
35      40      45

gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ctc ata      192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Leu Ile
50      55      60

gaa att tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca      240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr
65      70      75

cct gtc aac ata att gga aga aat ctg ttg acw cag att ggt tgc act      288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Xaa Gln Ile Gly Cys Thr
85      90      95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag      336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
100     105     110

cca gga atg gat ggc cca aga gtt aaa caa tgg cca ttg aca gaa gaa      384
Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu
115     120     125

aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aar gaa ggg      432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
130     135     140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca rta ttt      480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Xaa Phe
145     150     155     160

gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc      528
Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
165     170     175

aga gaa ctt aat aag agg act caa gat ttc tgg gaa gtt caa tta gga      576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
180     185     190

ata cca cat ccc gca ggg ttg aaa aag aaa aaa tca gta aca gta ctg      624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu
195     200     205

gat gtg ggt gat gca tat ttc tca gtt ccc tta gat gaa gac ttc aga      672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg
210     215     220

aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg      720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly
225     230     235     240

att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca      768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
245     250     255

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gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa	816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys	
260 265 270	
caa aat cca gac ata gtc atc tat caa tac atg gat gat ttg tat gta	864
Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val	
275 280 285	
gga tct gac tta gaa ata ggg cag cat agg aca aaa ata gag gaa ctg	912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu	
290 295 300	
aga caa cat ttg ttg aag tgg ggg ttt acc aca cca gac aaa aaa cat	960
Arg Gln His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His	
305 310 315 320	
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat	1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp	
325 330 335	
aaa tgg aca gtg cag cct ata gtg tta ccg gaa aaa gac agc tgg act	1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr	
340 345 350	
gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag	1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln	
355 360 365	
att tac cca ggg att	1119
Ile Tyr Pro Gly Ile	
370	

<210> 81
 <211> 1116
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)

<220>
 <221> CDS
 <222> (1)...(297)
 <223> HIV Protease

 <221> CDS
 <222> (298)...(1116)
 <223> Portion of HIV Reverse Transcriptase

<400> 81	
cct caa atc act ctt tgg caa cga ccy ctt gtt rcc ata aag ata ggg	48
Pro Gln Ile Thr Leu Trp Gln Arg Xaa Leu Val Xaa Ile Lys Ile Gly	
1 5 10 15	
ggg caa cta arg gaa gct cta tta gat aca gga gca gat gat aca gta	96
Gly Gln Leu Xaa Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val	
20 25 30	
tta gaa gaa ata aat ttg cca gga aga tgg aaa cca aaa atg ata ggg	144
Leu Glu Glu Ile Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly	
35 40 45	
gga att gga ggt ttt atc aaa gta aaa cag tat gat caa ata ccy rta	192
Gly Ile Gly Gly Phe Ile Lys Val Lys Gln Tyr Asp Gln Ile Xaa Xaa	
50 55 60	

gaa att tgt gga cat aga gct ata ggt aca gtw tta gta gga cct aca Glu Ile Cys Gly His Arg Ala Ile Gly Thr Xaa Leu Val Gly Pro Thr 65 70 75 80	240
cct gtc aac ata att gga agr aat ctg ttg act cag att ggt tgc act Pro Val Asn Ile Ile Gly Xaa Asn Leu Leu Thr Gln Ile Gly Cys Thr 85 90 95	288
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca ttg gta gaa att tgt aca gaa atg gaa aag gaa gga Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly 130 135 140	432
aaa att tca aga att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Arg Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gct ata aag aaa aar gat agt act aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528
agg gaa ctt aat aag agg act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gaa ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Glu Phe Arg 210 215 220	672
aag tat act gca ttt act ata cct agt aca aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly 225 230 235 240	720
att aga tat caa tac aat gtg ctt cca caa gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agt agc atg aca aaa atc tta gag cca ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gaa ata gtc atc tat caa tac gtg gat gat ttg tat gta Gln Asn Pro Glu Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac tta gaa ata gga cag cat aga aca aaa ata gag gaa yta Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Xaa 290 295 300	912
aga gaa cat ctg tta arg tgg gga ttt acc aca cca gac aaa aag cat Arg Glu His Leu Leu Xaa Trp Gly Phe Thr Thr Pro Asp Lys Lys His 305 310 315 320	960

cag aaa gaa cct cca ttt ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta cag cct ata cag ctg cca gaa aag gaa agc tgg act Lys Trp Thr Val Gln Pro Ile Gln Leu Pro Glu Lys Glu Ser Trp Thr 340 345 350	1056
gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
att tat gca ggg Ile Tyr Ala Gly 370	1116
 <210> 82 <211> 1116 <212> DNA <213> Human Immunodeficiency Virus (HIV)	
 <220> <221> CDS <222> (1)...(297) <223> HIV Protease	
 <221> CDS <222> (298)...(1116) <223> Portion of HIV Reverse Transcriptase	
 <400> 82	
cct cag atc act ctt tgg caa cga ccc ctc gtc aca gta aag ata ggg Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Val Lys Ile Gly 1 5 10 15	48
ggg caa tta aag gaa gct cta tta gat aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Thr Val 20 25 30	96
tta gaa gaa atg agt tta cca gga aaa tgg aaa cca aaa atg ata ggg Leu Glu Glu Met Ser Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly 35 40 45	144
gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ctt gta Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Leu Val 50 55 60	192
gaa atc tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr 65 70 75 80	240
ccc gtc aac ata att gga aga aat ctg ttg act cag att ggg tgc act Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr 85 90 95	288
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384

aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa ggg Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly 130 135 140	432
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gcc ata aaa aag aaa gac agt act aaa tgg aga aag tta gta gat ttc Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528
aga gaa ctt aay aaa aag act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gam ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Xaa Phe Arg 210 215 220	672
aar tat act gca ttt acc ata cct agt gta aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Val Asn Asn Glu Thr Pro Gly 225 230 235 240	720
att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttt caa agt agc atg aca aaa atc tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gac ata gtt atc tay cag tac atg gat gat ttg tat gta Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac tta gaa ata ggr aag cac aga aca aaa ata gag gag cta Gly Ser Asp Leu Glu Ile Xaa Lys His Arg Thr Lys Ile Glu Glu Leu 290 295 300	912
aga cag cat ctg ttg aag tgg gga ttt acc aca cca gac aaa aaa cat Arg Gln His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His 305 310 315 320	960
cag aaa gaa cct cca ttc ctk tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Xaa Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta cag cct ata aaa ctg cca gaa aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Lys Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056
gty aat gac ata cag aag tta gtg gga aaa ttr aat tgg gcc agt cag Xaa Asn Asp Ile Gln Lys Leu Val Gly Lys Xaa Asn Trp Ala Ser Gln 355 360 365	1104
att tat gca ggg Ile Tyr Ala Gly 370	1116

<210> 83
 <211> 1116
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)

<220>
 <221> CDS
 <222> (1)...(297)
 <223> HIV Protease

<221> CDS
 <222> (298)...(1116)
 <223> Portion of HIV Reverse Transcriptase

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<400> 83
cct cag atc act ctt tgg caa cga cca ctc gtc gca ata aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Ala Ile Lys Ile Gly
   1               5               10               15

ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
               20               25               30

tta gaa gac atg agt tta cca gga aaa tgg aaa cca aaa atg ata ggg      144
Leu Glu Asp Met Ser Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly
               35               40               45

gga att gga ggt ttt atc aaa gta aga cag tat gat caa gta ccc ata      192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Val Pro Ile
   50               55               60

gaa atc tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca      240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr
   65               70               75

cct gtc aac ata att gga aga aat ctg ttg act cag ctt ggt tgc act      288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr
               85               90               95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag      336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
               100               105               110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa      384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
               115               120               125

aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa gga      432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
               130               135               140

aaa att tca aaa att ggg cct gaa aat cca tat aat act cca gta ttt      480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
               145               150               155

gcc ata aag aaa aaa gac agt act aaa tgg agg aaa tta gta gat ttt      528
Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
               165               170               175

aga gaa ctt aat aag aga act caa gat ttc tgg gaa gtt caa tta gga      576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
               180               185               190

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ata cca cat cca gca ggg tta aaa aag aaa aag tca gta aca gtg ctg	624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu	
195 200 205	
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gaa ttc agg	672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Glu Phe Arg	
210 215 220	
aag tat act gca ttt acc ata ccc agt ata aac aat gag aca ccc agg	720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Arg	
225 230 235 240	
gtt aga tat caa tac aat gta ctt cca cag gga tgg aaa gga tca cca	768
Val Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro	
245 250 255	
gca tat ttc caa agt agc atg aca aaa atc tta gaa ccc ttc aga aaa	816
Ala Tyr Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys	
260 265 270	
caa aac cca gac ata gtt atc tat caa tac atg gat gac tta tat gta	864
Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val	
275 280 285	
gga tct gac tta gag ata gga cag cat aga gca aaa ata gag gac cta	912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Asp Leu	
290 295 300	
aga gca cat ctg ttg aag tgg ggg ttt acc aca cca gac aaa aaa cat	960
Arg Ala His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His	
305 310 315 320	
cag aaa gaa ccc cca ttt ctc tgg atg ggt tat gaa ctc cat cct gat	1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp	
325 330 335	
aaa tgg aca gta cag cct ata gwg cta cca gaa aaa gac agc tgg act	1056
Lys Trp Thr Val Gln Pro Ile Xaa Leu Pro Glu Lys Asp Ser Trp Thr	
340 345 350	
gtc aat gac ata cag aaa tta gta gga aaa tta aat tgg gca agt cag	1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln	
355 360 365	
att tat cca ggg	1116
Ile Tyr Pro Gly	
370	

<210> 84
 <211> 1116
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)

<220>
 <221> CDS
 <222> (1)...(297)
 <223> HIV Protease

<221> CDS
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 <223> Portion of HIV Reverse Transcriptase

<400> 84
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ggg caa cta atg gaa gct cta tta gat aca gga gca gat gat aca gta 96
 Gly Gln Leu Met Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
 20 25 30

tta gaa gac ata aat ttg cca gga aga tgg aaa cca aaa ata ata ggg 144
 Leu Glu Asp Ile Asn Leu Pro Gly Arg Trp Lys Pro Lys Ile Ile Gly
 35 40 45

gga att ggt ggt ttt gtc aaa gtg aga cag tat gat cag gta ccc ata 192
 Gly Ile Gly Gly Phe Val Lys Val Arg Gln Tyr Asp Gln Val Pro Ile
 50 55 60

gaa atc tgt gga cat aaa gtt ata ggt aca gta tta gta gga cct aca 240
 Glu Ile Cys Gly His Lys Val Ile Gly Thr Val Leu Val Gly Pro Thr
 65 70 75 80

cct acc aac gta gtt gga aga aat ctg atg act cag att ggc tgc acy 288
 Pro Thr Asn Val Val Gly Arg Asn Leu Met Thr Gln Ile Gly Cys Xaa
 85 90 95

tta aat ttt cct att agt cct att gaa act gta cca gta aaa tta aag 336
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
 100 105 110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg acg gaa gaa 384
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
 115 120 125

aaa ata aaa gca tta gta gaa att tgt aca gaa ctg gaa aag gat gga 432
 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Asp Gly
 130 135 140

aaa att tca aaa att ggg cct gaa aat cca tat aat act cca ata ttt 480
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe
 145 150 155 160

gcc ata aag aaa aag aac agt gat aaa tgg aga aaa tta gta gat ttc 528
 Ala Ile Lys Lys Lys Asn Ser Asp Lys Trp Arg Lys Leu Val Asp Phe
 165 170 175

aga gaa ctt aat aar aga act caa gac ttc tgg gaa gtt caa tta gga 576
 Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
 180 185 190

ata cca cat cct gca ggg tta aaa aag aat aaa tca gta aca gta ctg 624
 Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu
 195 200 205

gat ata ggt gat gca tat ttt tca att ccc tta gat aaa gac ttt agg 672
 Asp Ile Gly Asp Ala Tyr Phe Ser Ile Pro Leu Asp Lys Asp Phe Arg
 210 215 220

aag tat act gca ttc acc ata cct agt ata aac aat gag aca cca ggg 720
 Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly
 225 230 235 240

gtt aga tat cag tac aat gtg ctt cca cag gga tgg aag gga tca cca 768
 Val Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
 245 250 255

gca ata ttc caa agc agc atg acc aaa atc tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
cag aat cca gac ata gtt atc tgc caa tac gtg 'gat gat ttg tat gta Gln Asn Pro Asp Ile Val Ile Cys Gln Tyr Val Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctr Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Xaa 290 295 300	912
agg aat yat ctg tgg aag tgg gga ttt tac aca cca gac aaa aaa tat Arg Asn Xaa Leu Trp Lys Trp Gly Phe Tyr Thr Pro Asp Lys Lys Tyr 305 310 315 320	960
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta cag ccc ata gtg ctg cca gaa aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056
gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
att tat cca ggg Ile Tyr Pro Gly 370	1116
<210> 85	
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<212> DNA	
<213> Human Immunodeficiency Virus (HIV)	
<220>	
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<222> (1)...(297)	
<223> HIV Protease	
<221> CDS	
<222> (298)...(1116)	
<223> Portion of HIV Reverse Transcriptase	
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cct caa atc act ctt tgg caa cga ccc ctc gtc aca ata aaa gta ggg Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Val Gly 1 5 10 15	48
ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30	96
tta gaa gaa atg aat ttg cca ggg aga tgg aaa cca aaa atg ata ggg Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly 35 40 45	144
gga att gga ggt ttt atc aaa gta aga cag tat gat cag gta agc ata Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Val Ser Ile 50 55 60	192

gaa atc tgt gga cat aaa gct ata ggt aca gta tta ata gga ccc acc Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Ile Gly Pro Thr 65 70 75 80	240
cct gtc aac ata att gga aga aat ctg ttg act cag ctt ggt tgc act Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr 85 90 95	288
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aga gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gag aag gaa ggr Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Xaa 130 135 140	432
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gcc ata aar aaa aaa gac agt act aaa tgg aga aag tta gta gat ttc Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528
aga gaa ctt aat aaa ara act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Xaa Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat ccc gca ggg tta aaa aag aam aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Xaa Lys Ser Val Thr Val Leu 195 200 205	624
gay gtg ggt gat gcr tat ttt tca gtt ccy tta gay aaa gay ttc agg Asp Val Gly Asp Xaa Tyr Phe Ser Val Xaa Leu Asp Lys Asp Phe Arg 210 215 220	672
aag tac aca gca ttt acc ata cct agt gta aac aat gag rca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Val Asn Asn Glu Xaa Pro Gly 225 230 235 240	720
att aga tat cag tac aat gtg ctt cca car gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aar Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
maa aat cca gac ata gty atc tay caa tac atg gat gat ttr tat gta Xaa Asn Pro Asp Ile Xaa Ile Tyr Gln Tyr Met Asp Asp Xaa Tyr Val 275 280 285	864
gga tct gac tta gaa ata gga cag cat aga aca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300	912
aga caa cat ctg ttg cag tgg ggg tta acc aca cca gac aaa aaa cat Arg Gln His Leu Leu Gln Trp Gly Leu Thr Thr Pro Asp Lys Lys His 305 310 315 320	960

cag aaa gaa cct cca ttc ctt tgg atg ggg tat gaa ctc cat ccg gat	1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp	
325 330 335	
aaa tgg aca gta cag cct ata wtg ctg cca gac aaa gac agc tgg act	1056
Lys Trp Thr Val Gln Pro Ile Xaa Leu Pro Asp Lys Asp Ser Trp Thr	
340 345 350	
gtm aat gac ata cag aar tta gta gga aaa ttg aat tgg gcg agt cag	1104
Xaa Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln	
355 360 365	
atc tac cca ggg	1116
Ile Tyr Pro Gly	
370	
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<211> 1116	
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<222> (1)...(297)	
<223> HIV Protease	
<221> CDS	
<222> (298)...(1116)	
<223> Portion of HIV Reverse Transcriptase	
<400> 86	
cct caa atc act ctt tgg caa cga ccc atc gtc aca gta aag ata ggg	48
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1 5 10 15	
ggg cac aca acg gaa gct cta tta gat aca gga gca gat gat aca gta	96
Gly His Thr Thr Glu Ala Leu Leu Asp Thr Gly Ala Asp Thr Val	
20 25 30	
tta gaa gaa atg aat ttg cca ggg aga tgg aaa cca aaa atg ata gga	144
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly	
35 40 45	
gga att gga ggt ttt atc aaa gta aga cag tat gag cag gta ccc ata	192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Glu Gln Val Pro Ile	
50 55 60	
gaa ttc tgt gga cat aaa act gta ggt aca gta tta ata gga cct aca	240
Glu Phe Cys Gly His Lys Thr Val Gly Thr Val Leu Ile Gly Pro Thr	
65 70 75 80	
cct gtc aac ata att gga aga aat ctg atg act cag att ggt tgt act	288
Pro Val Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Ile Gly Cys Thr	
85 90 95	
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag	336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys	
100 105 110	
cca gga atg gat ggg ccc aaa gtt aaa cca tgg cca ttg aca gaa aga	384
Pro Gly Met Asp Gly Pro Lys Val Lys Pro Trp Pro Leu Thr Glu Arg	
115 120 125	

aaa aat aaa gca tta gta gaa att tgt tcc gaa atg gaa aaa gga agg Lys Asn Lys Ala Leu Val Glu Ile Cys Ser Glu Met Glu Lys Gly Arg 130 135 140	432
aaa att tca aaa att ggg cct gag aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gcc ata aag aaa aag aac agt act aga tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asn Ser Thr Arg Trp Arg Lys Leu Val Asp Phe 165 170 175	528
aga gaa ctt aat aaa aga act caa gac ttc tgg gaa gtt cag tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat ccc gca ggg tta aaa aag aac aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu 195 200 205	624
gat gta ggt gat gca tat ttt tca gtt ccc tta gat gaa gaa ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Glu Phe Arg 210 215 220	672
aag tat act gca ttc acc ata cct agt aca aac aat gaa aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly 225 230 235 240	720
att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa tgt agc atg aca aaa atc tta gag ccc ttt aga aaa Ala Ile Phe Gln Cys Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gaa ata gtt atc tgt cag tac atg gat gac ttg tat gta Gln Asn Pro Glu Ile Val Ile Cys Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864
gca tct gat tta gaa ata ggg cag cat aga aca aaa gta gag gaa ctg Ala Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Val Glu Glu Leu 290 295 300	912
aga caa cat ctg ttg aag tgg ggg ttt ttc aca cca gac gaa aaa cat Arg Gln His Leu Leu Lys Trp Gly Phe Phe Thr Pro Asp Glu Lys His 305 310 315 320	960
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta cag cct ata gta ctg cca gac caa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Asp Gln Asp Ser Trp Thr 340 345 350	1056
gtc aat gat ata cag aag tta gtg gga aaa tta aat tgg gca agt caa Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
att tac cca ggg Ile Tyr Pro Gly 370	1116

<210> 87
 <211> 1116
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)

<220>
 <221> CDS
 <222> (1)...(297)
 <223> HIV Protease

<221> CDS
 <222> (298)...(1116)
 <223> Portion of HIV Reverse Transcriptase

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 Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Glu
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ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta 96
 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
 20 25 30

tta gaa gaa atg aat ttg tca gga aga tgg aaa cca aaa atg ata ggg 144
 Leu Glu Glu Met Asn Leu Ser Gly Arg Trp Lys Pro Lys Met Ile Gly
 35 40 45

gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ccc ata 192
 Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile
 50 55 60

gag atc tgt gga cat aaa gct gta ggt aca gta tta gta gga cct aca 240
 Glu Ile Cys Gly His Lys Ala Val Gly Thr Val Leu Val Gly Pro Thr
 65 70 75 80

cct gtc aac ata att gga agr aat ctg ttg act cag att ggt tgc acc 288
 Pro Val Asn Ile Ile Gly Xaa Asn Leu Leu Thr Gln Ile Gly Cys Thr
 85 90 95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
 100 105 110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
 115 120 125

aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa ggg 432
 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
 130 135 140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca ata ttt 480
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe
 145 150 155 160

gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat tty 528
 Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
 165 170 175

aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga 576
 Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
 180 185 190

ata cca cat ccy gca ggg ttg aar aag aaa aaa tca gta aca gta ctg Ile Pro His Xaa Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttc tca gtt ccc tta gat gaa gay ttc aga Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg 210 215 220	672
aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240	720
gtt aga tat car tac aat gtg ctt cca cag gga tgg aag gga tca cca Val Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agc agc atg aca aaa atc tta gag cct ttt agg aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gat ata gtt atc tat caa tac atg gat gac ttr tat gta Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Xaa Tyr Val 275 280 285	864
gga tct gac tta gaa ata ggg car cat aga aca aaa ata gag gaa ttg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300	912
aga caa cat ctg ttg aag tgg gga tta acc aca cca gac aaa aaa cat Arg Gln His Leu Leu Lys Trp Gly Leu Thr Thr Pro Asp Lys Lys His 305 310 315 320	960
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056
gtc aat gat ata cag aag tta gtg gga aaa tta aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
att tat gca ggg Ile Tyr Ala Gly 370	1116

<210> 88
 <211> 1116
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)

<220>
 <221> CDS
 <222> (1)...(297)
 <223> HIV Protease

<221> CDS
 <222> (298)...(1116)
 <223> Portion of HIV Reverse Transcriptase

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<400> 88
cct cag atc act ctt tgg caa cga ccc atc gtc aca ata aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Ile Gly
  1           5           10           15

ggg caa cta agg raa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Arg Xaa Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
          20           25           30

tta gaa gac ata gaa ttg cca gga aga tgg aaa cca aaa atg ata ggg      144
Leu Glu Asp Ile Glu Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
          35           40           45

gga att gga ggt ttt gtc aaa gta aga caa tat gat cag ata ccc ata      192
Gly Ile Gly Gly Phe Val Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile
          50           55           60

gaa atc tgt gga cat aaa gtt ata ggt aca gta tta gta gga cct aca      240
Glu Ile Cys Gly His Lys Val Ile Gly Thr Val Leu Val Gly Pro Thr
          65           70           75           80

cct gcc aac ata att gga aga aat ctg atg act cag ctt ggt tgc act      288
Pro Ala Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Leu Gly Cys Thr
          85           90           95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag      336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
          100          105          110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca aaa gaa      384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Lys Glu
          115          120          125

aaa ata gaa gca tta atr gaa att tgt gma ttt ttg gaa aag gaa gga      432
Lys Ile Glu Ala Leu Xaa Glu Ile Cys Xaa Phe Leu Glu Lys Glu Gly
          130          135          140

aaa att tca aaa att ggg cct gaa aat ccg tac aac act cca gta ttt      480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
          145          150          155          160

gcc ata aag aaa aaa gga ggt act aaa tgg aga aaa ata gta gat ttc      528
Ala Ile Lys Lys Lys Gly Gly Thr Lys Trp Arg Lys Ile Val Asp Phe
          165          170          175

aga gaa ctt aat aaa aga act caa gac ttc tgg gaa gtt caa tta gga      576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
          180          185          190

ata cca cat ccc gcg ggg tta aaa aag aay aaa tca gta aca gta ctg      624
Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu
          195          200          205

gat gtg ggt gat gca tat ttt tca att ccc tta gat gaa gaa ctc agg      672
Asp Val Gly Asp Ala Tyr Phe Ser Ile Pro Leu Asp Glu Glu Leu Arg
          210          215          220

aag tat act gca ttt act ata cct agt aca aac aat gag aca cca ggg      720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly
          225          230          235          240

att aga tac caa tac aat gtg ctt cca cag gga tgg aaa gga tca cca      768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
          245          250          255

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gca ata ttt caa agt agc atg aca aaa atc tta gag ccc ttt aga aag 816
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 260 265 270

caa aat cca gac ata gtt atc twt caw tac gtg gat gat ttg tat gta 864
 Gln Asn Pro Asp Ile Val Ile Xaa Xaa Tyr Val Asp Asp Leu Tyr Val
 275 280 285

gga tct gac tta gaa ata ggg aag cat agg gaa aaa ata gag gaa ctg 912
 Gly Ser Asp Leu Glu Ile Gly Lys His Arg Glu Lys Ile Glu Glu Leu
 290 295 300

aga caa cat ctg tgg aag tgg gga ttt tac aca cca gac gaa aaa cat 960
 Arg Gln His Leu Trp Lys Trp Gly Phe Tyr Thr Pro Asp Glu Lys His
 305 310 315 320

cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat ctt gat 1008
 Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Leu Asp
 325 330 335

aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act 1056
 Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
 340 345 350

gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt cag 1104
 Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
 355 360 365

att tat gca ggg 1116
 Ile Tyr Ala Gly
 370

<210> 89
 <211> 1116
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)

<220>
 <221> CDS
 <222> (1)...(297)
 <223> HIV Protease

<221> CDS
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 <223> Portion of HIV Reverse Transcriptase

<400> 89
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 Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly
 1 5 10 15

ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta 96
 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
 20 25 30

tta gaa gaa atg agt ttg cca ggg aga tgg aaa cca aaa atg ata ggg 144
 Leu Glu Glu Met Ser Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
 35 40 45

gga att gga ggt ttt atc aaa gta aga caa ttt gat cag ata ccc ata 192
 Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Phe Asp Gln Ile Pro Ile
 50 55 60

gaa ata tgt gga cac aaa gct ata ggt aca gta tta ata gga cct aca Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Ile Gly Pro Thr 65 70 75 80	240
cct gtc aac ata att gga agg aat ctg ttg act cag ctt ggt tgc act Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr 85 90 95	288
tta aat ttt ccc atc agt cct att gaa cct gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Pro Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta gta gaa att tgt aca gaa ctg gaa aaa gaa ggg Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly 130 135 140	432
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca ata ttt Lys Ile Ser Lys Ile Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe 145 150 155 160	480
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528
aga gaa ctg aat aag aaa act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta acg gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg 210 215 220	672
aaa tat act gca ttt acc ata cct agt aca aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly 225 230 235 240	720
att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttt caa cat agc atg aca aaa atc tta gag cct ttt aga aaa Ala Ile Phe Gln His Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
cag aat cca gac ata gtt atc tat caa tac gtg gat gac ttg tat gta Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300	912
aga gaa cat ctg ttg aag tgg gga ttt tac aca cca gac aaa aaa cat Arg Glu His Leu Leu Lys Trp Gly Phe Tyr Thr Pro Asp Lys Lys His 305 310 315 320	960

cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat	1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp	
325 330 335	
aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act	1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr	
340 345 350	
gtc aat gat ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag	1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln	
355 360 365	
att tat gca ggg	1116
Ile Tyr Ala Gly	
370	
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<223> HIV Protease	
<221> CDS	
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<223> Portion of HIV Reverse Transcriptase	
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1 5 10 15	
gga cag cta aag gaa gct yta tta gat aca gga gca gat gat aca gta	96
Gly Gln Leu Lys Glu Ala Xaa Leu Asp Thr Gly Ala Asp Thr Val	
20 25 30	
tta gaa gaa atg aac ttg cca gga aaa tgg aaa cca aaa ata ata ggg	144
Leu Glu Glu Met Asn Leu Pro Gly Lys Trp Lys Pro Lys Ile Ile Gly	
35 40 45	
gga att gga ggt ttt gtc aga gta aga caa tat gat cag gta cct gta	192
Gly Ile Gly Gly Phe Val Arg Val Arg Gln Tyr Asp Gln Val Pro Val	
50 55 60	
gaa att tgt gga cat aaa gct ata ggt tca gta tta gta gga cca aca	240
Glu Ile Cys Gly His Lys Ala Ile Gly Ser Val Leu Val Gly Pro Thr	
65 70 75 80	
cct gcc aac ata att gga aga aat ctg atg act cag ctt ggt ttc act	288
Pro Ala Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Leu Gly Phe Thr	
85 90 95	
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag	336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys	
100 105 110	
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa	384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu	
115 120 125	

aaa ata aaa gca tta gta gar att tgt aca gaa ytg gaa aaa gaa gga Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Xaa Glu Lys Glu Gly 130 135 140	432
aag att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gcc ata aag aaa aag aac agt gat aga tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asn Ser Asp Arg Trp Arg Lys Leu Val Asp Phe 165 170 175	528
aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat cct gga ggg tta aaa aag aaa aaa tca gta aca gta cta Ile Pro His Pro Gly Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttc tca gtt ccc tta gat gaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg 210 215 220	672
aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240	720
att aga tat car tac aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata tty caa agt agc atg aca aaa atc tta gag cct ttt agg aag Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
maa aat cca gac ata gtt atc att caa tac atg gat gat ttg tat gtr Xaa Asn Pro Asp Ile Val Ile Gln Tyr Met Asp Asp Leu Tyr Xaa 275 280 285	864
gga tct gat tta gaa ata gar cag cay aga aca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300	912
aga gat cat tta ttg agg tgg ggg ttt ttc aca cca gaa caa aaa cat Arg Asp His Leu Leu Arg Trp Gly Phe Phe Thr Pro Glu Gln Lys His 305 310 315 320	960
cag aaa gaa cct cca ttc cat tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe His Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta cat cct ata gtg ctg cca gaa aaa gac agc tgg act Lys Trp Thr Val His Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056
gtc aat gac ata cag aag tta gtg gga aaa ttr aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Xaa Asn Trp Ala Ser Gln 355 360 365	1104
att tat gca ggg Ile Tyr Ala Gly 370	1116

<210> 91
 <211> 1115
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)

<220>
 <221> CDS
 <222> (1)...(297)
 <223> HIV Protease

<221> CDS
 <222> (298)...(1115)
 <223> Portion of HIV Reverse Transcriptase

<400> 91
 cct cag atc act ctt tgg caa cga ccc ctt gtc aca gta aag ata ggg 48
 Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Val Lys Ile Gly
 1 5 10 15
 ggg caa cta ata gaa gct cta tta gat aca gga gca gat gat aca gta 96
 Gly Gln Leu Ile Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
 20 25 30
 ttg gaa gaa atg aat ttg cca ggg aga tgg aaa cca aaa ata ata ggg 144
 Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Ile Ile Gly
 35 40 45
 gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ccc ata 192
 Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile
 50 55 60
 gaa atc tgt gga cat aaa gtt ata rgt cca gta tta ata gga cct aca 240
 Glu Ile Cys Gly His Lys Val Ile Xaa Pro Val Leu Ile Gly Pro Thr
 65 70 75 80
 cct gtc aac ata att gga aga aat ttg atg act cag att ggc tgc act 288
 Pro Val Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Ile Gly Cys Thr
 85 90 95
 tta aat ttt ccc atc agt cct att raa act gta cca gta aaa tta aag 336
 Leu Asn Phe Pro Ile Ser Pro Ile Xaa Thr Val Pro Val Lys Leu Lys
 100 105 110
 cca gga atg gat ggc cca aag gtt aaa caa tgg cca ttg aca gaa gaa 384
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
 115 120 125
 aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa gga 432
 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
 130 135 140
 aaa atc tca aaa att ggg cct gaa aac cca tac aat act cca gta ttt 480
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
 145 150 155 160
 gcc ata aag aaa aaa aac agt act aga tgg aga aaa tta gta gat ttc 528
 Ala Ile Lys Lys Lys Asn Ser Thr Arg Trp Arg Lys Leu Val Asp Phe
 165 170 175
 aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga 576
 Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
 180 185 190

ata cca cat cct gga ggg tta aaa aag aaa aaa tca gta aca gta ctg	624
Ile Pro His Pro Gly Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu	
195 200 205	
gat gtg ggt gat gca tat ttt tca gtt cct cta gat gaa gac ttc agg	672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg	
210 215 220	
aag tat act gca ttt acc ata cct agt ata aat aat gag aca cca ggg	720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly	
225 230 235 240	
gtt aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tcg cca	768
Val Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro	
245 250 255	
gca ata ttt cag gct agc atg aca aaa atc tta gag ccg ttt aga aaa	816
Ala Ile Phe Gln Ala Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys	
260 265 270	
caa aat cca gac ata gtt atc tat caa tac gtg gat gat ttg tat gta	864
Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val	
275 280 285	
gga tct gac cta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg	912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu	
290 295 300	
aga caa cat ttg ttg aaa tgg gga ttt atc aca cca gat gaa aaa cat	960
Arg Gln His Leu Leu Lys Trp Gly Phe Ile Thr Pro Asp Glu Lys His	
305 310 315 320	
cag aaa gaa cct cca ttc ctt tgg atg ggg tat gaa ctc cat cct gat	1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp	
325 330 335	
aag tgg aca gta cag cct ata gta ctg cca gaa aaa gac agc tgg act	1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr	
340 345 350	
gtc aat gac ata cag aaa tta gtg gga aaa ttg aat tgg gca agt cag	1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln	
355 360 365	
att tat gca gg	1115
Ile Tyr Ala	
370	

<210> 92
 <211> 1116
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)

<220>
 <221> CDS
 <222> (1)...(297)
 <223> HIV Protease

<221> CDS
 <222> (298)...(1116)
 <223> Portion of HIV Reverse Transcriptase

<400> 92
 cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata aag ata ggg 48
 Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly
 1 5 10 15

ggg cag cta aag gaa gct cta tta gat aca gga gca gat gat aca gta 96
 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
 20 25 30

tta gaa gac ata aac ttg cca gga aaa tgg aaa cca aaa atg ata ggg 144
 Leu Glu Asp Ile Asn Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly
 35 40 45

gga att gga ggt ttt atc aaa gta aga cag tat gag cag gta ccc ata 192
 Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Glu Gln Val Pro Ile
 50 55 60

gaa atc tgt gga cat aaa act ata ggt aca gta tta gta gga cct aca 240
 Glu Ile Cys Gly His Lys Thr Ile Gly Thr Val Leu Val Gly Pro Thr
 65 70 75 80

cct gtc aac ata att gga aga aat ctg atg act cag att ggg tgc act 288
 Pro Val Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Ile Gly Cys Thr
 85 90 95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
 100 105 110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
 115 120 125

aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa ggg 432
 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
 130 135 140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt 480
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
 145 150 155 160

gcc ata aag aaa aag aac agt act aga tgg aga aaa gta gta gat ttc 528
 Ala Ile Lys Lys Lys Asn Ser Thr Arg Trp Arg Lys Val Val Asp Phe
 165 170 175

aga gaa ctt aat aag aaa act caa gac ttc tgg gaa gtt caa tta gga 576
 Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
 180 185 190

ata cca cat ccc gca ggg tta aaa aag aac aaa tca gta aca gta ctg 624
 Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu
 195 200 205

gat gtg ggt gat gca tat ttt tca gtt ccc tta gat gaa gac ttc agg 672
 Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg
 210 215 220

aag tat act gca ttt acc ata cct agt ata aac aat gag acg cca ggg 720
 Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly
 225 230 235 240

att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca 768
 Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
 245 250 255

gca ata ttc caa agt agc atg aca aaa ata tta gag cct ttt aga aaa	816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys	
260 265 270	
caa aat cca gac ctg gtt atc tgt caa tac atg gat gat tta tat gta	864
Gln Asn Pro Asp Leu Val Ile Cys Gln Tyr Met Asp Asp Leu Tyr Val	
275 280 285	
gga tct gac cta gaa ata ggg cag cat aga aca aaa ata gaa gaa ctg	912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu	
290 295 300	
agg caa cat ctg ttg aag tgg gga ttt acc aca cca gac gaa aaa cat	960
Arg Gln His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Glu Lys His	
305 310 315 320	
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat	1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp	
325 330 335	
aaa tgg aca gta cag ccc ata gtg ctg cca gac aaa gac agc tgg act	1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Asp Lys Asp Ser Trp Thr	
340 345 350	
gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag	1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln	
355 360 365	
att tat gca ggg	1116
Ile Tyr Ala Gly	
370	

<210> 93
 <211> 1116
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)

<220>
 <221> CDS
 <222> (1)...(297)
 <223> HIV Protease

 <221> CDS
 <222> (298)...(1116)
 <223> Portion of HIV Reverse Transcriptase

<400> 93	
cct cag atc act ctt tgg caa cga ccc atc gtc aca ata aag ata gga	48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Ile Gly	
1 5 10 15	
ggg cag cta aag gaa gct cta ata gat aca gga gca gat gat aca gta	96
Gly Gln Leu Lys Glu Ala Leu Ile Asp Thr Gly Ala Asp Asp Thr Val	
20 25 30	
tta gaa gaa atg aat tta cca gga aga tgg aca cca aaa ata ata ggg	144
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Thr Pro Lys Ile Ile Gly	
35 40 45	
gga att gga ggt ttt gtc aga gta aga cag tat gaa cag ata ccc gta	192
Gly Ile Gly Gly Phe Val Arg Val Arg Gln Tyr Glu Gln Ile Pro Val	
50 55 60	

gaa atc tgc ggg cat aaa gct gta ggt aca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Ala Val Gly Thr Val Leu Val Gly Pro Thr 65 70 75 80	240
cct gcc aac ata att gga aga aat ctg ttg act cag att ggc tgt act Pro Ala Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr 85 90 95	288
tta aat ttt ccc att agt cct att gat act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Asp Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca ara gtt aaa caa tgg cca ttg aca gaa gag Pro Gly Met Asp Gly Pro Xaa Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta gta gaa att tgt aca gaa ctg gaa aag gam gga Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Xaa Gly 130 135 140	432
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gct ata aag aaa aaa gac agt act aaa tgg aga aaa gta gta gat ttc Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Val Val Asp Phe 165 170 175	528
aga gaa ctt aat aaa aga act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat cct gca ggg ata maa aag aac aaa tca gta aca gta ytg Ile Pro His Pro Ala Gly Ile Xaa Lys Asn Lys Ser Val Thr Val Xaa 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat gag gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg 210 215 220	672
aag tac act gca ttt acc ata cct agt aca aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly 225 230 235 240	720
att aga tat cag tac aat gta ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agt agc atg aca aaa aty tta gag cct ttt aga aag Ala Ile Phe Gln Ser Ser Met Thr Lys Xaa Leu Glu Pro Phe Arg Lys 260 265 270	816
aaa aat cca gac ata rtt atc tgc caa tac atg gat gat ttg tat gta Lys Asn Pro Asp Ile Xaa Ile Cys Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac tta gaa ata gag cag cat aga aca aaa ata gat gaa ctg Gly Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Asp Glu Leu 290 295 300	912
aga gac cat ctg tgg aag tgg gga ttt tac aca cca gac aac aaa yat Arg Asp His Leu Trp Lys Trp Gly Phe Tyr Thr Pro Asp Asn Lys Xaa 305 310 315 320	960

cag aaa gaa cct cca ttc cgt tgg atg ggc tat gaa ctc cat cct gat 1008
 Gln Lys Glu Pro Pro Phe Arg Trp Met Gly Tyr Glu Leu His Pro Asp
 325 330 335

aaa tgg aca gta cag cct ata gtg ctg cca gaa aag gat agc tgg act 1056
 Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
 340 345 350

gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag 1104
 Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
 355 360 365

aat tat gca gga 1116
 Asn Tyr Ala Gly
 370

<210> 94
 <211> 1116
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)

<220>
 <221> CDS
 <222> (1)...(297)
 <223> HIV Protease

<221> CDS
 <222> (298)...(1116)
 <223> Portion of HIV Reverse Transcriptase

<400> 94
 cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata aag ata ggg 48
 Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly
 1 5 10 15

ggg caa cta ata gag gct cta ttg gat aca gga gca gat gat aca gta 96
 Gly Gln Leu Ile Glu Ala Leu Leu Asp Thr Gly Ala Asp Thr Val
 20 25 30

tta gaa gaa atg gat ttg cca gga aga tgg aaa cca aaa ata ata ggg 144
 Leu Glu Glu Met Asp Leu Pro Gly Arg Trp Lys Pro Lys Ile Ile Gly
 35 40 45

gga att gga ggt tgg atc aaa gta aga caa tat gat cag ata ccc ata 192
 Gly Ile Gly Gly Trp Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile
 50 55 60

gaa att tgt gga cat aaa gtt ata agt aca gta tta gta gga cct aca 240
 Glu Ile Cys Gly His Lys Val Ile Ser Thr Val Leu Val Gly Pro Thr
 65 70 75 80

cca gtc aac gta att gga aga aat ctg atg act cag att ggt tgc act 288
 Pro Val Asn Val Ile Gly Arg Asn Leu Met Thr Gln Ile Gly Cys Thr
 85 90 95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
 100 105 110

cca gga atg gat ggc cca aga gtt aaa caa tgg cca ttg aca gaa gaa 384
 Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu
 115 120 125

aag ata aaa gca tta gta gaa att tgt aca gaa ttg gaa aag gat ggg Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Asp Gly 130 135 140	432
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa gta gta gat ttc Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Val Val Asp Phe 165 170 175	528
aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta ggg Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat ccc gca ggg tta cca aag aaa aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Pro Lys Lys Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat gaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg 210 215 220	672
aaa tat act gca ttt acc ata cct agt ata aat aat gag aca cca gga Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240	720
gtt aga tat cag tac aat gtg ctc cca cag ggg tgg aaa gga tca cca Val Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agt agc atg acc aaa atc tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
cag aat cca aac ata ctt att tgt caa tac atg gat gat ttg tat gta Gln Asn Pro Asn Ile Leu Ile Cys Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac tta gaa ata gaa cag cat aga aca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300	912
aga caa cat ctg tgg aga tgg ggg ttt tac aca cca gat aaa aaa cat Arg Gln His Leu Trp Arg Trp Gly Phe Tyr Thr Pro Asp Lys Lys His 305 310 315 320	960
cag aag gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta cag cct ata gag ctg cca gaa aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Glu Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056
gtc aat gat ata cag aag tta gtg gga aaa ttg aat tgg gca agy cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Xaa Gln 355 360 365	1104
att tat gca ggg Ile Tyr Ala Gly 370	1116

<210> 95
 <211> 1116
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)

<220>
 <221> CDS
 <222> (1)...(297)
 <223> HIV Protease

<221> CDS
 <222> (298)...(1116)
 <223> Portion of HIV Reverse Transcriptase

<400> 95
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 1 5 10 15
 ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta 96
 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
 20 25 30
 tta gaa gaa atg aat ttg cca gga agg tgg aaa cca aaa atg ata ggg 144
 Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
 35 40 45
 gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata tcc gta 192
 Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Ser Val
 50 55 60
 gaa atc tgt ggr cat aaa gct ata ggt aca gta tta rta gga cct aca 240
 Glu Ile Cys Xaa His Lys Ala Ile Gly Thr Val Leu Xaa Gly Pro Thr
 65 70 75 80
 cct gtc aac ata att gga agg aat ttg ttg act cag att ggt tgc act 288
 Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
 85 90 95
 tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
 100 105 110
 cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
 115 120 125
 aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa gga 432
 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
 130 135 140
 aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt 480
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
 145 150 155 160
 gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc 528
 Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
 165 170 175
 aga gaa ctt aat aag aaa act caa gac ttt tgg gar gtt caa tta gga 576
 Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
 180 185 190

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ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta ctg      624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu
      195                                200                                205

gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg      672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg
      210                                215                                220

aag tac act gca ttt act ata cct agt ata aac aat gag aca cca ggg      720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly
      225                                230                                235

att aga tat caa tac aat gtg ctt cca cag gga tgg aaa gga tca cca      768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
      245                                250                                255

gca ata ttc cag tgt agc atg aca aaa atc tta gag cct ttt aga aaa      816
Ala Ile Phe Gln Cys Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys
      260                                265                                270

caa aat cca gar ata gtt atc tat caa tac atg gat gat ctg tat gta      864
Gln Asn Pro Glu Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val
      275                                280                                285

gga tct gac tta gaa ata gaa cag cat aga ata aaa ata gag gaa ctg      912
Gly Ser Asp Leu Glu Ile Glu Gln His Arg Ile Lys Ile Glu Glu Leu
      290                                295                                300

aga cac cat ctg ttg aaa tgg gga ttt wmc aca cca gac aaa aaa cat      960
Arg His His Leu Leu Lys Trp Gly Phe Xaa Thr Pro Asp Lys Lys His
      305                                310                                315

cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat      1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
      325                                330                                335

aaa tgg aca gta cag cct ata gtg ctg cca gaa aar gac agc tgg act      1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
      340                                345                                350

gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt cag      1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
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att tac cca ggg
Ile Tyr Pro Gly
      370

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<211> 1116
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<213> Human Immunodeficiency Virus (HIV)

<220>
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<222> (1) ... (297)
<223> HIV Protease

<221> CDS
<222> (298) ... (1116)
<223> Portion of HIV Reverse Transcriptase

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 1 5 10 15

ggg caa cta agg gaa gct cta tta gat aca gga gca gat gat aca gta 96
 Gly Gln Leu Arg Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
 20 25 30

tta gaa gaa ata aat ttg cca gga aga tgg aaa cca aaa atg ata ggg 144
 Leu Glu Glu Ile Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
 35 40 45

gga att ggg ggt ttt atc aaa gta aga sag tat gat cag gta ccc gta 192
 Gly Ile Gly Gly Phe Ile Lys Val Arg Xaa Tyr Asp Gln Val Pro Val
 50 55 60

gaa atc tgt gga cat aaa gct ata ggt aca gta tta gta gga ccc aca 240
 Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr
 65 70 75 80

cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act 288
 Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
 85 90 95

tta aat ttt ccc att agt cct att gaa act gta cca gta ara tta aag 336
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Xaa Leu Lys
 100 105 110

cca ggr atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384
 Pro Xaa Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
 115 120 125

aaa ata aaa gca tta gta gaa atc tgt aca gaa atg gaa aag gaa ggg 432
 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
 130 135 140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca ata ttt 480
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe
 145 150 155 160

gcc ata aag aaa aaa gac ggt act aaa tgg aga aaa gta gta gat ttc 528
 Ala Ile Lys Lys Lys Asp Gly Thr Lys Trp Arg Lys Val Val Asp Phe
 165 170 175

agg gaa ctc aat aag aga act caa gac ttc tgg gaa gtt caa tta ggm 576
 Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Xaa
 180 185 190

ata cca cat ccc gca ggg ttg aaa aag aaa aaa tca gtr aca gta ctg 624
 Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Xaa Thr Val Leu
 195 200 205

gat gtg ggt gat gca tat ttt tca gtt ccc tta gat gaa gaa ttc agg 672
 Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Glu Phe Arg
 210 215 220

aag tat act gca ttt acc ata cct agt gta aac aat gag aca cca ggg 720
 Lys Tyr Thr Ala Phe Thr Ile Pro Ser Val Asn Asn Glu Thr Pro Gly
 225 230 235 240

atc aga tat caa tac aat gtg ctt cca cag gga tgg aag gga tca cca 768
 Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
 245 250 255

gca ata ttt caa agt agc atg aca aaa atc tta gag cct ttt aga aaa	816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys	
260 265 270	
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Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val	
275 280 285	
gga tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg	912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu	
290 295 300	
aga caa cat ctg ttg aag tgg gga ttt acc aca cca gac aaa aaa cat	960
Arg Gln His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His	
305 310 315 320	
cag aaa gag cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat	1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp	
325 330 335	
aaa tgg aca gta cag cgt ata gag ctg cca gaa aag gag agc tgg act	1056
Lys Trp Thr Val Gln Arg Ile Glu Leu Pro Glu Lys Glu Ser Trp Thr	
340 345 350	
gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt caa	1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln	
355 360 365	
atw tac cca ggg	1116
Xaa Tyr Pro Gly	
370	

<210> 97
 <211> 1116
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)

<220>
 <221> CDS
 <222> (1)...(297)
 <223> HIV Protease

<221> CDS
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 <223> Portion of HIV Reverse Transcriptase

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1 5 10 15	
ggg caa ata aag gaa gcy tta tta gat aca gga gca gat gat aca gtg	96
Gly Gln Ile Lys Glu Xaa Leu Leu Asp Thr Gly Ala Asp Asp Thr Val	
20 25 30	
tta gaa gaa atg aat ttg cca gga aaa tgg aaa cca aaa ttg ata ggg	144
Leu Glu Glu Met Asn Leu Pro Gly Lys Trp Lys Pro Lys Leu Ile Gly	
35 40 45	
gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ctt ata	192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Leu Ile	
50 55 60	

gaa atc tgt ggc cat aaa gct ata ggt aca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr 65 70 75 80	240
cct gcc aac ata att gga aga aat ctg ttg act cag att ggt tgc act Pro Ala Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr 85 90 95	288
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta cta gaa att tgt aca gaa ctg gaa aag gaa ggg Lys Ile Lys Ala Leu Leu Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly 130 135 140	432
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528
aga gaa ctt aat aag aga act caa gac ttt tgg gag gtt caa cta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
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gat gtg ggt gat gca tat ttt tca gtt ccc tta tat gag gac tty agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Tyr Glu Asp Phe Arg 210 215 220	672
aaa tat act gca ttt act ata cct agt aca aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly 225 230 235 240	720
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cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat	1008
Gln Lys Glu Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp	
325 330 335	
aaa tgg aca gta cag cct ata gta ctg cca gaa aaa gac agc tgg act	1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr	
340 345 350	
gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag	1104
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att tac cca ggg	1116
Ile Tyr Pro Gly	
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1 5 10 15	
ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta	96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val	
20 25 30	
tta gaa gaa atg cat ttg cca gga aaa tgg aaa cca aaa atg ata ggg	144
Leu Glu Glu Met His Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly	
35 40 45	
gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata cct gta	192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Val	
50 55 60	
gaa aty tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca	240
Glu Xaa Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr	
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Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr	
85 90 95	
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag	336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys	
100 105 110	
cca ggg atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa	384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu	
115 120 125	

aaa ata aaa gca tta gta gaa ata tgt aca gaa atg gaa aag gaa ggg Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly 130 135 140	432
aaa att tca aaa att ggg cca gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528
aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa ttg gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat ccc gca gga tta aaa aag aaa aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg 210 215 220	672
aag tac act gca ttt acc ata cct agt ata aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240	720
att aga tat cag tat aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gay ata gtt att tat caa tac atg gat gat ttg tat gta Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864
gga tcc gac cta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300	912
aga caa cac ctg ttg aag tgg ggr ttt acc ack cca gac aaa aaa cat Arg Gln His Leu Leu Lys Trp Xaa Phe Thr Xaa Pro Asp Lys Lys His 305 310 315 320	960
cag aag gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta cag cct ata gta ctg cca gaa aaa gat agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056
gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
att tac tca gt Ile Tyr Ser 370	1115

<210> 99
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<220>
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 <222> (1)...(297)
 <223> HIV Protease

<221> CDS
 <222> (298)...(1115)
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 1 5 10 15
 ggg caa cta aag gaa gct yta tta gat aca gga gca gat gat aca gta 96
 Gly Gln Leu Lys Glu Ala Xaa Leu Asp Thr Gly Ala Asp Thr Val
 20 25 30
 tta gaa gaa atg aat ttg cca gga agr tgg aaa cca aaa atg ata ggg 144
 Leu Glu Glu Met Asn Leu Pro Gly Xaa Trp Lys Pro Lys Met Ile Gly
 35 40 45
 gga att gga ggc ttt atc aaa gta aga cag tat gat cag ata ccc cta 192
 Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Leu
 50 55 60
 gaa atc tgt ggc cat aag gct ata ggt aca gta tta gta gga cct aca 240
 Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr
 65 70 75 80
 cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act 288
 Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
 85 90 95
 tta aat ttt ccc att agt cct att gaa act gta cct gta aaa tta aag 336
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
 100 105 110
 cca gga atg gat ggt cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
 115 120 125
 aaa ata aaa gca tta gta gaa att tgt aca gag atg gaa aag gaa ggg 432
 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
 130 135 140
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 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
 145 150 155 160
 gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc 528
 Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
 165 170 175
 aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga 576
 Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
 180 185 190

ata cca cat ccc tca ggg tta raa aag aag aaa tca gta aca gta ctg	624
Ile Pro His Pro Ser Gly Leu Xaa Lys Lys Lys Ser Val Thr Val Leu	
195 200 205	
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat cca gat ttc agg	672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Pro Asp Phe Arg	
210 215 220	
aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg	720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly	
225 230 235 240	
att agg tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca	768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro	
245 250 255	
gca ata ttc caa agc agc atg aca aaa atc tta gag cct ttt aga aaa	816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys	
260 265 270	
caa aat cca gaa ata gtt atc tac caa tac dtg gat gat ttg tak gta	864
Gln Asn Pro Glu Ile Val Ile Tyr Gln Tyr Xaa Asp Asp Leu Xaa Val	
275 280 285	
rgc tct gac tta gaa ata ggg cag cat aga gca aaa ata gag gaa ctg	912
Xaa Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Leu	
290 295 300	
aga caa cat ctg ttg agg tgg gga ttt acc aca cca gac aaa aag cat	960
Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His	
305 310 315 320	
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat	1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp	
325 330 335	
aaa tgg aca gtt cag cct ata gtg ctg cca gaa aag gac agc tgg act	1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr	
340 345 350	
gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag	1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln	
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att tat gca gg	1115
Ile Tyr Ala	
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<210> 100
 <211> 1115
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)

 <220>
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 <222> (1) ... (297)
 <223> HIV Protease

 <221> CDS
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 <223> Portion of HIV Reverse Transcriptase

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ggg cag ctr aag gaa gct ata tta gat aca gga gca gat gat aca kta Gly Gln Xaa Lys Glu Ala Ile Leu Asp Thr Gly Ala Asp Asp Thr Xaa 20 25 30	96
tta gaa gaa atg aat tng ccc gga aga tgg ama cca ama ttg ata ggg Leu Glu Glu Met Asn Xaa Pro Gly Arg Trp Xaa Pro Xaa Leu Ile Gly 35 40 45	144
gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ccc ata Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile 50 55 60	192
gaa atc tgt gga cat aaa gtt ata ggt aca gta ttg gta gga cct aca Glu Ile Cys Gly His Lys Val Ile Gly Thr Val Leu Val Gly Pro Thr 65 70 75 80	240
cct acc aac ata att gga aga aat ctg atg act cag ctt ggt tgc act Pro Thr Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Leu Gly Cys Thr 85 90 95	288
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta gta gaa att tgt aca gaa ttg gaa aag gaa ggg Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly 130 135 140	432
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528
aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca ata ctg Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Ile Leu 195 200 205	624
gat gtg ggc gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg 210 215 220	672
aaa gta tac tgc ttt acc ata cct agt ata acc aat gag acm cca ggg Lys Val Tyr Cys Phe Thr Ile Pro Ser Ile Thr Asn Glu Xaa Pro Gly 225 230 235 240	720
att aga tat cag tac aat gtg ctg cca caa gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768

gca ata ttc caa agt agc atg aca aaa atc tta gag ccy ttt aga aaa	816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Xaa Phe Arg Lys	
260 265 270	
caa aat cca gac ata gtt atc tat caa tac gtg gat gat ttg tat gta	864
Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val	
275 280 285	
gga tct gac tta gaa ata ggg cag cat aga gca aaa ata gag gaa ctg	912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Leu	
290 295 300	
aga caa cat ctg tgg agg tgg gga ttt tac aca cca gac aaa aaa cat	960
Arg Gln His Leu Trp Arg Trp Gly Phe Tyr Thr Pro Asp Lys Lys His	
305 310 315 320	
cag aag gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat	1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp	
325 330 335	
aaa tgg aca gta cag cct ata arg ttg cca gaa aaa gac agc tgg act	1056
Lys Trp Thr Val Gln Pro Ile Xaa Leu Pro Glu Lys Asp Ser Trp Thr	
340 345 350	
gtc aat gam ata cag aaa tta gtg gga aaa tta aat tgg gcc agt cag	1104
Val Asn Xaa Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln	
355 360 365	
att tck cng gg	1115
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<210> 101
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Pro Gln Ile Thr Leu Trp Gln Thr Pro Leu Val Xaa Ile Arg Xaa Gly	
1 5 10 15	
ggr cag yta aag gaa gct tta tta gay aca gra gca gat gat mca gta	96
Xaa Gln Xaa Lys Glu Ala Leu Leu Asp Thr Xaa Ala Asp Asp Xaa Val	
20 25 30	
tta gaa gaa atg tat ttg cca gga aga tgg aaa cca aaa atg ata ggg	144
Leu Glu Glu Met Tyr Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly	
35 40 45	
gga att gga ggt ttt atc aag gta aga cag tat gat cag ata ccc ata	192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile	
50 55 60	

gaa atc tgt gga cac aaa gct ata ggt aca gta ttg gta gga tct aca Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Ser Thr 65 70 75 80	240
cct gtt aac ata att gga aga aat ctg ttg act cag att ggt tgc acc Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr 85 90 95	288
tta aat ttt ccc att agt tct att gaa act gta cca gta aga tta aag Leu Asn Phe Pro Ile Ser Ser Ile Glu Thr Val Pro Val Arg Leu Lys 100 105 110	336
ccc gga atg gat ggc cca aaa gtt aag caa tgg cca tta aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa ggg Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly 130 135 140	432
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gcc ata aag aaa aag aac agt gat aga tgg aga aaa gta gta gat ttc Ala Ile Lys Lys Lys Asn Ser Asp Arg Trp Arg Lys Val Val Asp Phe 165 170 175	528
aga gaa ctt aat aag aga acc caa gac ttt tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat ccc gca ggg tta aaa agg aga aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Arg Arg Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tac ttt tca att ccc tta gat aaa gaa ttc aga Asp Val Gly Asp Ala Tyr Phe Ser Ile Pro Leu Asp Lys Glu Phe Arg 210 215 220	672
aag tat act gca ttt acc ata cct agt aca aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly 225 230 235 240	720
atc aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga gaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Glu 260 265 270	816
cag aat cca gac atg gtt atc tat caa tac atg gat gat ttg tat gta Gln Asn Pro Asp Met Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac tta gaa ata ggg cag cat aga gca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Leu 290 295 300	912
aga caa cat ctg ttg agg tgg gga tta ttc aca cca gac caa aaa cat Arg Gln His Leu Leu Arg Trp Gly Leu Phe Thr Pro Asp Gln Lys His 305 310 315 320	960

cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat ccg gat 1008
 Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
 325 330 335

aaa tgg aca gta cag act ata gtg ctg cca gag aag gac agc tgg act 1056
 Lys Trp Thr Val Gln Thr Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
 340 345 350

gtc aat gac ata cag aag tta gta gga aaa ttg aat tgg g 1096
 Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp
 355 360 365

<210> 102
 <211> 1048
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)

<220>
 <221> CDS
 <222> (1)...(297)
 <223> HIV Protease

<221> CDS
 <222> (298)...(1048)
 <223> Portion of HIV Reverse Transcriptase

<400> 102
 cct cag atc act ctt tgg cag cga ccc tty gtc aca ata aag gta ggg 48
 Pro Gln Ile Thr Leu Trp Gln Arg Pro Phe Val Thr Ile Lys Val Gly
 1 5 10 15

ggg caa cta aag gaa gct cta ttg gat aca gga gca gat gat aca ata 96
 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Ile
 20 25 30

tta gaa gaa atg tgt ttg cca gga aga ttg aaa cca aaa ttg ata ggg 144
 Leu Glu Glu Met Cys Leu Pro Gly Arg Trp Lys Pro Lys Leu Ile Gly
 35 40 45

gga att gga ggt ttt gtc aaa gta aga caa tat gat cag ata ccc ata 192
 Gly Ile Gly Gly Phe Val Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile
 50 55 60

gaa atc tgt gga cat aaa gtt ata ggt aca gta tta gta gga cct aca 240
 Glu Ile Cys Gly His Lys Val Ile Gly Thr Val Leu Val Gly Pro Thr
 65 70 75 80

cct gcc aac ata gtt gga aga aat ctg ttg act cag att ggc tgt act 288
 Pro Ala Asn Ile Val Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
 85 90 95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
 100 105 110

cca gga atg gat ggg cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Thr Glu Glu
 115 120 125

aaa ata aaa gca tta gta gaa att tgt aca gaa ttg gag aag gat gga 432
 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Asp Gly
 130 135 140

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aaa att tca aaa att ggg cct gaa aat cca tay aat act cca gta ttt      480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
145                               150                               155                               160

gcc ata aag aaa aaa aat agt gat aaa tgg aga aaa gta gta gat ttc      528
Ala Ile Lys Lys Lys Asn Ser Asp Lys Trp Arg Lys Val Val Asp Phe
                               165                               170                               175

aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtc caa tta gga      576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
                               180                               185                               190

ata cca cat ccc gga ggg tta rag aag aac aaa tca ata aca gta ctg      624
Ile Pro His Pro Gly Gly Leu Xaa Lys Asn Lys Ser Ile Thr Val Leu
                               195                               200                               205

gat gtg ggt gat gca tat ttt tca att ccc tta gat aaa gac ttc aga      672
Asp Val Gly Asp Ala Tyr Phe Ser Ile Pro Leu Asp Lys Asp Phe Arg
                210                               215                               220

aag tat act gca ttt acc ata ccy agt ata aac aat gag aca cca ggg      720
Lys Tyr Thr Ala Phe Thr Ile Xaa Ser Ile Asn Asn Glu Thr Pro Gly
225                               230                               235                               240

att aga tat cag tat aat gtg ctt cca cag gga tgg aag gga tca cca      768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
                               245                               250                               255

gcc ata ttc caa agt agc atg aca aaa ata tta gag cct ttt aga aag      816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys
                               260                               265                               270

caa aat cca gac ata att atc gtt caa tac gtg gat gat ttg tat gta      864
Gln Asn Pro Asp Ile Ile Ile Val Gln Tyr Val Asp Asp Leu Tyr Val
                275                               280                               285

gca tct gac tta gaa ata ggg cag cat aga aca aaa ata aag gaa cta      912
Ala Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Lys Glu Leu
                290                               295                               300

aga caa tat ctg tgg gag tgg gga ttt tac aca cca gac aaa aaa cat      960
Arg Gln Tyr Leu Trp Glu Trp Gly Phe Tyr Thr Pro Asp Lys Lys His
305                               310                               315                               320

caa cag gaa ccc cca ttc ctc tgg atg ggg tat gag ctc cat cct gat     1008
Gln Gln Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
                               325                               330                               335

aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac a                1048
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp
                340                               345

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<210> 103
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (1) ... (297)
<223> HIV Protease

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<221> CDS

<222> (298) ... (1116)

<223> Portion of HIV Reverse Transcriptase

<400> 103

cct	cag	atc	act	ctt	tgg	caa	cga	ccc	ctc	gtc	aca	ata	arg	rta	ggg	48
Pro	Gln	Ile	Thr	Leu	Trp	Gln	Arg	Pro	Leu	Val	Thr	Ile	Xaa	Xaa	Gly	
1				5					10						15	
ggg	cag	cta	aag	gaa	gct	cta	tta	gat	aca	gga	gca	gat	gat	aca	gta	96
Gly	Gln	Leu	Lys	Glu	Ala	Leu	Leu	Asp	Thr	Gly	Ala	Asp	Asp	Thr	Val	
			20					25					30			
tta	gaa	gaa	atg	aat	ttg	cca	gga	aga	tgg	aaa	cca	aaa	atg	ata	ggg	144
Leu	Glu	Glu	Met	Asn	Leu	Pro	Gly	Arg	Trp	Lys	Pro	Lys	Met	Ile	Gly	
			35				40					45				
gga	att	gga	ggg	ttt	atc	aaa	gta	aga	cag	tat	gat	cag	ata	ccc	ata	192
Gly	Ile	Gly	Gly	Phe	Ile	Lys	Val	Arg	Gln	Tyr	Asp	Gln	Ile	Pro	Ile	
	50					55					60					
gaa	atc	tgt	gga	cat	aaa	gct	gaa	ggg	aca	gta	tta	gta	gga	cct	aca	240
Glu	Ile	Cys	Gly	His	Lys	Ala	Glu	Gly	Thr	Val	Leu	Val	Gly	Pro	Thr	
	65				70				75						80	
ccg	gtc	aac	ata	att	gga	aga	aat	ctg	ttg	act	cag	att	ggg	tgc	act	288
Pro	Val	Asn	Ile	Ile	Gly	Arg	Asn	Leu	Leu	Thr	Gln	Ile	Gly	Cys	Thr	
				85				90						95		
tta	aat	ttt	ccc	att	agt	cct	att	gaa	act	gta	cca	gta	aaa	tta	aag	336
Leu	Asn	Phe	Pro	Ile	Ser	Pro	Ile	Glu	Thr	Val	Pro	Val	Lys	Leu	Lys	
			100					105					110			
cca	gga	atg	gat	ggc	cca	aaa	gtt	aaa	caa	tgg	cca	ctg	aca	gaa	gaa	384
Pro	Gly	Met	Asp	Gly	Pro	Lys	Val	Lys	Gln	Trp	Pro	Leu	Thr	Glu	Glu	
		115					120					125				
aaa	ata	aaa	gca	tta	aba	gaa	att	tgt	aca	gaa	atg	gaa	aag	gaa	ggr	432
Lys	Ile	Lys	Ala	Leu	Xaa	Glu	Ile	Cys	Thr	Glu	Met	Glu	Lys	Glu	Xaa	
	130					135					140					
aaa	att	tca	aaa	att	ggg	cct	gaa	aat	cca	tac	aat	act	ccg	gta	ttt	480
Lys	Ile	Ser	Lys	Ile	Gly	Pro	Glu	Asn	Pro	Tyr	Asn	Thr	Pro	Val	Phe	
	145				150					155					160	
gcc	ata	aag	aaa	aaa	gac	agt	act	aaa	tgg	aga	aaa	tta	gta	gat	ttc	528
Ala	Ile	Lys	Lys	Lys	Asp	Ser	Thr	Lys	Trp	Arg	Lys	Leu	Val	Asp	Phe	
				165					170					175		
aga	gaa	ctt	aat	aag	aaa	act	caa	gac	ttt	tgg	gaa	gtt	caa	tta	gga	576
Arg	Glu	Leu	Asn	Lys	Lys	Thr	Gln	Asp	Phe	Trp	Glu	Val	Gln	Leu	Gly	
			180					185					190			
ata	cca	cac	ccc	gca	ggg	tta	aaa	aag	aaa	aaa	tca	gta	aca	gta	ctg	624
Ile	Pro	His	Pro	Ala	Gly	Leu	Lys	Lys	Lys	Lys	Ser	Val	Thr	Val	Leu	
		195					200					205				
gat	gtg	ggg	gat	gca	tat	ttt	tca	gtt	ccc	tta	gat	aaa	gaa	ttc	agg	672
Asp	Val	Gly	Asp	Ala	Tyr	Phe	Ser	Val	Pro	Leu	Asp	Lys	Glu	Phe	Arg	
	210					215					220					
aag	tat	aca	gca	ttt	acc	ata	cct	agt	aca	aac	aat	gag	aca	ccc	agg	720
Lys	Tyr	Thr	Ala	Phe	Thr	Ile	Pro	Ser	Thr	Asn	Asn	Glu	Thr	Pro	Arg	
	225				230					235					240	

att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tcg cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gac ata gtt atc tat caa tat gtg gat gat ttg tat gta Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac tta gag ata ggg cag cat aga aca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300	912
aga saa cat ctg ttg agg tgg gga ttt acc aca cca gac aaa aaa cat Arg Xaa His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His 305 310 315 320	960
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gtr cag cct ata rag ctg cca gaa aaa gac agc tgg act Lys Trp Thr Xaa Gln Pro Ile Xaa Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056
gtc aat gac ata cag aaa tta gtg gga aaa tta aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
att tac gca gga Ile Tyr Ala Gly 370	1116

<210> 104
 <211> 1116
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)

<220>
 <221> CDS
 <222> (1)...(297)
 <223> HIV Protease

<221> CDS
 <222> (298)...(1116)
 <223> Portion of HIV Reverse Transcriptase

<400> 104 cct cag atc act ctt tgg caa cga ccc mty gtc aca ata aag gta ggg Pro Gln Ile Thr Leu Trp Gln Arg Pro Xaa Val Thr Ile Lys Val Gly 1 5 10 15	48
ggg caa tta aaa gaa gct cta tta gat aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30	96
cta gaa gaa ata aat ttg cca gga aga tgg aaa cca aaa atg ata ggg Leu Glu Glu Ile Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly 35 40 45	144

gga att gga ggt ttt atc aaa gta aga cag tat gat car ata cyt ata Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Xaa Ile 50 55 60	192
gaa atc tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr 65 70 75 80	240
cct gtc aac ata att gga aga aat ctg ttr act cag att ggc tgc act Pro Val Asn Ile Ile Gly Arg Asn Leu Xaa Thr Gln Ile Gly Cys Thr 85 90 95	288
tta aat ttt ccc ata agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta gya gaa att tgt aca gaa atg gaa aag gaa gga Lys Ile Lys Ala Leu Xaa Glu Ile Cys Thr Glu Met Glu Lys Glu Gly 130 135 140	432
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gct ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528
aga gaa ctt aat aag aga act caa gac ttt tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat cca gca ggg cta cca agg aaa aga tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Pro Arg Lys Arg Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat cca gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Pro Asp Phe Arg 210 215 220	672
aag tat act gca ttt acc ata cct agt ata aac aat gag aca ccg ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240	720
att aga tat cag tac aat gta ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gcc ata ttc caa agt agc atg aca aaa att tta gat cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Asp Pro Phe Arg Lys 260 265 270	816
caa aat cca gac ata att atc tat caa tac gtg gat gat ttg tat gta Gln Asn Pro Asp Ile Ile Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val 275 280 285	864
gca tct gac tta gaa ata ggg cag cac aga aca aaa ata gaa gaa cta Ala Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300	912

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aga caa cat ctg ttg agg tgg gga ttt tac aca cca gac aaa aaa cat      960
Arg Gln His Leu Leu Arg Trp Gly Phe Tyr Thr Pro Asp Lys Lys His
305                      310                      315                      320

cag aaa gaa cct cca ttt ctt tgg atg ggt tat gaa ctc cat cct gat      1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
                      325                      330                      335

aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act      1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
                      340                      345                      350

gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag      1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
                      355                      360                      365

att tat gca ggg
Ile Tyr Ala Gly
                      370

<210> 105
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

<400> 105
cct cag atc act ctt tgg caa cga ccc ttc gtc gtc gta aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Phe Val Val Val Lys Ile Gly
1                      5                      10                      15

ggg caa cta aag gaa gct cta tta gat aca gga gca gat aat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asn Thr Val
                      20                      25                      30

ttt gaa gac ytg aat ttg cca gga aaa tgg aaa cca aaa atg ata ggg      144
Phe Glu Asp Xaa Asn Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly
                      35                      40                      45

gga att gga ggt ttt atc aaa gta aga cag tat gat cag gta ctt gta      192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Val Leu Val
50                      55                      60

gaa atc tgt gga caa aaa gct ata ggt aca gta tta ata gga cct aca      240
Glu Ile Cys Gly Gln Lys Ala Ile Gly Thr Val Leu Ile Gly Pro Thr
65                      70                      75                      80

cct gtc aac ata att gga agg gat ctg ttg act cag att ggt tgc act      288
Pro Val Asn Ile Ile Gly Arg Asp Leu Leu Thr Gln Ile Gly Cys Thr
                      85                      90                      95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag      336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
100                      105                      110

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cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa	384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu	
115 120 125	
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa ggg	432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly	
130 135 140	
aar att tca aaa att ggg cct gaa aac cca tac aat act cca gta ttt	480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe	
145 150 155 160	
gcc ata aag aaa aaa gac agt act aar tgg aga aaa tta gta gat ttc	528
Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe	
165 170 175	
aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga	576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly	
180 185 190	
ata cca cat cct gca ggg tta aaa aag aaa aaa tca gta aca gta ctg	624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu	
195 200 205	
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat gaa gay' ttc agg	672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg	
210 215 220	
aag tat act gca ttt acc ata cct agc ata aac aat gag aca cca gga	720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly	
225 230 235 240	
att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca	768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro	
245 250 255	
gca ata ttc caa tgt agc atg aca aaa atc tta gat cct ttt aga aag	816
Ala Ile Phe Gln Cys Ser Met Thr Lys Ile Leu Asp Pro Phe Arg Lys	
260 265 270	
caa aat cca gac cta gtt atc tat caa tac rtg gat gac ttg tat gta	864
Gln Asn Pro Asp Leu Val Ile Tyr Gln Tyr Xaa Asp Asp Leu Tyr Val	
275 280 285	
gga tct gat tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg	912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu	
290 295 300	
aga car cat ctg ttg aag tgg gga ttt acc aca cca gac aaa aar cat	960
Arg Gln His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His	
305 310 315 320	
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat	1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp	
325 330 335	
aaa tgg aca gta cag cct ata gtg ctg cca gaa aag gac agc tgg act	1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr	
340 345 350	
gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag	1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln	
355 360 365	

att tac cca ggg
 ile Tyr Pro Gly
 370

1116

<210> 106
 <211> 1116
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)

<220>
 <221> CDS
 <222> (1)...(297)
 <223> HIV Protease

<221> CDS
 <222> (298)...(1116)
 <223> Portion of HIV Reverse Transcriptase

<400> 106
 cct cag atc act ctt ngg caa cga ccm att gtc aca ata aag gta ggg 48
 Pro Gln Ile Thr Leu Xaa Gln Arg Xaa Ile Val Thr Ile Lys Val Gly
 1 5 10 15

ggg cam tta aaa gaa gtt ytt tta gat mma gga gca gat gat cma gta 96
 Gly Xaa Leu Lys Glu Val Xaa Leu Asp Xaa Gly Ala Asp Asp Xaa Val
 20 25 30

tta gaa gaa atr gat ttg cca gga aga tgg aaa cca aaa atg ata ggg 144
 Leu Glu Glu Xaa Asp Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
 35 40 45

gga att gga ggt ttt atc aaa gta aga cag tat gat caa ata gtt gta 192
 Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Val Val
 50 55 60

gaa atc tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca 240
 Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr
 65 70 75 80

cct gtc aac ata att gga aga aat ctg ttg act cag ctt ggt tgc act 288
 Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr
 85 90 95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
 100 105 110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gag gaa 384
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
 115 120 125

aaa ata aaa gca ttg gta gaa att tgt aca gaa atg gaa aag gaa gga 432
 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
 130 135 140

aaa att tca aaa aty ggg cct gaa aat cca tac aat act cca gta ttt 480
 Lys Ile Ser Lys Xaa Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
 145 150 155 160

gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc 528
 Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
 165 170 175

agg gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat ccc gca ggg yta aaa aag aac aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Xaa Lys Lys Asn Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttc tca gtt ccc tta gat aaa gac ttt agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg 210 215 220	672
aag tat act gca ttt acc ata ccc agt ata aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240	720
att aga tat cag tat aat gtg ctt cca caa gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agt agc atg aca aaa atc cta gag cct ttt agg aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gac ata gtt atc tat caa tac atg gat gat ttg tat gta Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac tta gaa ata ggg cag cat aga aca aaa ata gaa gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300	912
aga gca cat ctg tta aag tgg gga ttt acc aca cca gay aaa aag cat Arg Ala His Leu Leu Lys Trp Gly Phe Thr Pro Asp Lys Lys His 305 310 315 320	960
cag aaa gaa cct cca ttt ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gtg cag cct ata aag ctg cca gaa aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Lys Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056
gtc aat gat ata cag aag tta gtg gga aaa ttg aat tgg gcc agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
att tat cca gga Ile Tyr Pro Gly 370	1116

<210> 107

<211> 1116

<212> DNA

<213> Human Immunodeficiency Virus (HIV)

<220>

<221> CDS

<222> (1) ... (297)

<223> HIV Protease

<221> CDS

<222> (298)...(1116)

<223> Portion of HIV Reverse Transcriptase

<400> 107

cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata aag ata ggg	48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly	
1 5 10 15	
ggg caa cta aag gaa gct tta tta gat aca gga gca gat gat aca gta	96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val	
20 25 30	
tta gaa gaa atg gaa ttg cca gga aga tgg aaa cca aaa atg ata ggg	144
Leu Glu Glu Met Glu Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly	
35 40 45	
gga att gga ggt ttt atc aaa gta agm cag tat gat cag ata ccc ata	192
Gly Ile Gly Gly Phe Ile Lys Val Xaa Gln Tyr Asp Gln Ile Pro Ile	
50 55 60	
gaa att tgt gga cat aaa gct gtg ggt aca gta tta gta gga cct aca	240
Glu Ile Cys Gly His Lys Ala Val Gly Thr Val Leu Val Gly Pro Thr	
65 70 75 80	
cct gtc aac ata att gga aga aat ctg ttg act aag att ggt tgc act	288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Lys Ile Gly Cys Thr	
85 90 95	
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag	336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys	
100 105 110	
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa	384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu	
115 120 125	
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa gga	432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly	
130 135 140	
aaa att tca aaa att gga cct gaa aat cca tac aat act cca gta ttt	480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe	
145 150 155 160	
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc	528
Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe	
165 170 175	
aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga	576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly	
180 185 190	
ata cca cat ccc gca ggg tta aaa mgg aaa aaa tca gta aca gta ctg	624
Ile Pro His Pro Ala Gly Leu Lys Xaa Lys Lys Ser Val Thr Val Leu	
195 200 205	
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gag ttc agg	672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Glu Phe Arg	
210 215 220	
aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca gga	720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly	
225 230 235 240	

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att aga tat cag tac aat gtg yyt cca cag gga tgg aaa gga tca cca      768
Ile Arg Tyr Gln Tyr Asn Val Xaa Pro Gln Gly Trp Lys Gly Ser Pro
                245                250                255

gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa      816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys
                260                265                270

caa aat cca gaa ata gtt atc tat cag tac atg gat gat ttg tat gta      864
Gln Asn Pro Glu Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val
                275                280                285

gga tct gac tta gaa ata ggg cag cac aga aca aaa ata gag gaa ctg      912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu
                290                295                300

aga caa cat ctg ttg aag tgg gga ttt acc aca cca gac aaa aaa cat      960
Arg Gln His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His
305                310                315                320

cag aaa gaa ccc cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat     1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
                325                330                335

aaa tgg aca gta cag cct ata gtg cta cca gaa aaa gac agc tgg act     1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
                340                345                350

gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gcg agt cag     1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
355                360                365

att tay gca ggg
Ile Tyr Ala Gly
370

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<210> 108
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

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<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

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<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

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<400> 108
cct caa atc act ctt tgg caa cga ccc ctc gtc aca ata aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly
1                5                10                15

ggg cag cta aag gaa gct cta tta gat aca gga gca gat gat aca gtg      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
                20                25                30

tta gaa gaa atg aat ttg cca ggg aaa tgg aag cca aaa atg ata ggg     144
Leu Glu Glu Met Asn Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly
35                40                45

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gga att gga ggg ttt atc aaa gta agm crg tat gat cag ata ccc ata Gly Ile Gly Gly Phe Ile Lys Val Xaa Xaa Tyr Asp Gln Ile Pro Ile 50 55 60	192
gaa atc tgt gra cat aaa gct aya ggt aca gta tta ata ggm cct act Glu Ile Cys Xaa His Lys Ala Xaa Gly Thr Val Leu Ile Xaa Pro Thr 65 70 75 80	240
cct gtc aac ata att gga aga awt ctg atg act cag att ggg tgc act Pro Val Asn Ile Ile Gly Arg Xaa Leu Met Thr Gln Ile Gly Cys Thr 85 90 95	288
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gag Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa ggg Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly 130 135 140	432
aag att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gct ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528
aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat cct gca ggt tta aaa aag aaa aaa tca gta aca gta cta Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggg gat gca tat ttt tca gtt ccc tta gat gaa aac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asn Phe Arg 210 215 220	672
aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240	720
att aga tat cag tac aat gta ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa tgt agc atg aca aaa atc tta gag cct ttc aga aag Ala Ile Phe Gln Cys Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gaa atg gtt atc trc caa tac gtg gat gay ttg tat gta Gln Asn Pro Glu Met Val Ile Xaa Gln Tyr Val Asp Asp Leu Tyr Val 275 280 285	864
ggt tct gac tta gaa ata ggg cag cat aga gca aaa ata gag gaa ctr Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Xaa 290 295 300	912

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aga caa cat ctg ttg agg tgg gga ttt acc aca cca gac aaa aaa cat      960
Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His
305                               310                               315                               320

cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctm cat cct gat      1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Xaa His Pro Asp
                               325                               330                               335

aaa tgg aca gtg cag cat ata gaa ctg cca gaa caa gag agc tgg act      1056
Lys Trp Thr Val Gln His Ile Glu Leu Pro Glu Gln Glu Ser Trp Thr
                               340                               345                               350

gtc aat gac ata cag aag tta gtg gga aaa yta aat tgg gca agy cag      1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Xaa Asn Trp Ala Xaa Gln
                               355                               360                               365

att tat gca ggg
Ile Tyr Ala Gly
                               370

<210> 109
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

<400> 109
cct caa atc act ctt tgg caa cga ccc atc gtc aca gta aag ata gag      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Val Lys Ile Glu
1                               5                               10                               15

ggg cag cta aag gaa gct yta tta gat aca gga gca gat aat aca gta      96
Gly Gln Leu Lys Glu Ala Xaa Leu Asp Thr Gly Ala Asp Asn Thr Val
                               20                               25                               30

ttg gam gaa ata aat ttg cca gga aga tgg aaa cca aaa atg ata ggg      144
Leu Xaa Glu Ile Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
                               35                               40                               45

gga att gra ggt ttt atc aaa gta aam cag tat gat sag ata mcc ata      192
Gly Ile Xaa Gly Phe Ile Lys Val Xaa Gln Tyr Asp Xaa Ile Xaa Ile
                               50                               55                               60

gac atc tgt gga cat aaa gta ata ggt aca ata tta gta gga cct aca      240
Asp Ile Cys Gly His Lys Val Ile Gly Thr Ile Leu Val Gly Pro Thr
65                               70                               75                               80

cct gtc aac ata att gga aga gat ctg ttg act cag att ggc tgc act      288
Pro Val Asn Ile Ile Gly Arg Asp Leu Leu Thr Gln Ile Gly Cys Thr
                               85                               90                               95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag      336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
                               100                               105                               110

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cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gar gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta gta gaa att tgt aca gaa ttg gaa aag gaa gga Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly 130 135 140	432
aag att tca aaa att ggg cct gaa aat cca tac aac act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gcc ata aag aaa aag gac agt act aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528
aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat cct gca ggg tta aaa aag aaa aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat tty tca gtt ccc tta gmt aaa gaa tnn nnn Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Xaa Lys Glu Xaa Xaa 210 215 220	672
nnn nnn nnn nnn nnn nnn nnn nnn nnn nnn nnn nnn nnn nnn nnn Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa 225 230 235 240	720
nnn nnn nnn nnn nnn nnn nnn nnn cca cag gga tgg aaa gga tca cca Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gaa ata gtt atc tac car tac rtg gat gay ttg ttw gta Gln Asn Pro Glu Ile Val Ile Tyr Gln Tyr Xaa Asp Asp Leu Xaa Val 275 280 285	864
gga tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300	912
aga caa cat ctg ttg agg tgg gga ttt acc aca cca gac aaa aaa cat Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His 305 310 315 320	960
cag aaa gaa cct cca ttc ctt tgg atg ggy tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Xaa Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056
gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104

att tat cca ggg
 ile Tyr Pro Gly
 370

1116

<210> 110

<211> 1116

<212> DNA

<213> Human Immunodeficiency Virus (HIV)

<220>

<221> CDS

<222> (1)...(297)

<223> HIV Protease

<221> CDS

<222> (298)...(1116)

<223> Portion of HIV Reverse Transcriptase

<400> 110

cyt cag atc act ctt tgg caa cga ccc cts gtc aca ata aag gta ggg 48
 Xaa Gln ile Thr Leu Trp Gln Arg Pro Xaa Val Thr ile Lys Val Gly

1

5

10

15

ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta 96
 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val

20

25

30

tta gaa gaa atr aat ttg cca ggr aaa tgg aaa cca awa atg ata ggg 144
 Leu Glu Glu Xaa Asn Leu Pro Xaa Lys Trp Lys Pro Xaa Met ile Gly

35

40

45

gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ctc ata 192
 Gly ile Gly Gly Phe ile Lys Val Arg Gln Tyr Asp Gln ile Leu ile

50

55

60

gaa atc tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca 240
 Glu ile Cys Gly His Lys Ala ile Gly Thr Val Leu Val Gly Pro Thr

65

70

75

80

cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act 288
 Pro Val Asn ile ile Gly Arg Asn Leu Leu Thr Gln ile Gly Cys Thr

85

90

95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336
 Leu Asn Phe Pro ile Ser Pro ile Glu Thr Val Pro Val Lys Leu Lys

100

105

110

cca ggg atg gat ggc cca aaa gtt aag caa tgg cca ttg aca gaa gaa 384
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu

115

120

125

aaa ata aaa gca tta ata gaa atc tgt aca gaa atg gaa aag gaa gga 432
 Lys ile Lys Ala Leu ile Glu ile Cys Thr Glu Met Glu Lys Glu Gly

130

135

140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt 480
 Lys ile Ser Lys ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe

145

150

155

160

gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc 528
 Ala ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe

165

170

175


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aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga      576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
      180      185      190

ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gtg aca gta ctg      624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu
      195      200      205

gat gtg ggt gat gca tat ttt tca gtt ccc tta gat gaa gac ttc agg      672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg
      210      215      220

aag tac act gca ttt mcc ata cct agt ata aac aat gag aca cca ggg      720
Lys Tyr Thr Ala Phe Xaa Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly
      225      230      235      240

att aga tat cag tac aat gtg ctt cca caa gga tgg aaa gga tca cca      768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
      245      250      255

gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa      816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys
      260      265      270

caa mat cca gac atg gty atc tat caa tac atg gat gat ttg tat gta      864
Gln Xaa Pro Asp Met Xaa Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val
      275      280      285

gga tct gac tta gaa ata ggr cag cat aga gca aaa ata gag gaa ctg      912
Gly Ser Asp Leu Glu Ile Xaa Gln His Arg Ala Lys Ile Glu Glu Leu
      290      295      300

aga cag cat ttg ttg aag tgg gga ttt acc aca cca gac aaa aag cat      960
Arg Gln His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His
      305      310      315      320

cag aaa gag cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat      1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
      325      330      335

aaa tgg aca gta cag cct ata gag ctg cca gaa aar gam agc tgg act      1056
Lys Trp Thr Val Gln Pro Ile Glu Leu Pro Glu Lys Xaa Ser Trp Thr
      340      345      350

gtc aat gac ata cag aaa ata gtg gga aaa ttg aat tgg gca agt cag      1104
Val Asn Asp Ile Gln Lys Ile Val Gly Lys Leu Asn Trp Ala Ser Gln
      355      360      365

att tac cca ggg
Ile Tyr Pro Gly
      370

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<210> 111
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

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<220>
<221> CDS
<222> (1) ... (297)
<223> HIV Protease

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<221> CDS

<222> (298)...(1116)

<223> Portion of HIV Reverse Transcriptase

<400> 111

cct	cag	atc	act	ctt	tgg	caa	cga	ccc	ctc	gtc	aca	ata	aag	ata	ggg	48
Pro	Gln	Ile	Thr	Leu	Trp	Gln	Arg	Pro	Leu	Val	Thr	Ile	Lys	Ile	Gly	
1				5					10					15		
ggg	caa	ata	aag	gaa	gct	cta	tta	gat	aca	gga	gca	gat	gat	aca	gta	96
Gly	Gln	Ile	Lys	Glu	Ala	Leu	Leu	Asp	Thr	Gly	Ala	Asp	Asp	Thr	Val	
			20					25					30			
tta	gaa	gaa	atg	agc	ttg	cca	gga	aaa	tgg	aaa	cca	aaa	atg	ata	ggg	144
Leu	Glu	Glu	Met	Ser	Leu	Pro	Gly	Lys	Trp	Lys	Pro	Lys	Met	Ile	Gly	
			35				40					45				
gga	att	gga	ggg	ttt	atc	aaa	gta	agm	cag	tat	gwt	cat	ata	ccc	ata	192
Gly	Ile	Gly	Gly	Phe	Ile	Lys	Val	Xaa	Gln	Tyr	Xaa	His	Ile	Pro	Ile	
	50					55					60					
gaa	wtc	tgt	ggm	cat	aaa	gct	gaa	ggg	aca	gta	tta	ata	gga	cct	aca	240
Glu	Xaa	Cys	Xaa	His	Lys	Ala	Glu	Gly	Thr	Val	Leu	Ile	Gly	Pro	Thr	
65					70					75					80	
cct	gtc	aac	ata	att	gga	aga	aat	ctg	ttg	act	cag	ctt	ggg	tgc	act	288
Pro	Val	Asn	Ile	Ile	Gly	Arg	Asn	Leu	Leu	Thr	Gln	Leu	Gly	Cys	Thr	
				85					90					95		
tta	aat	ttt	ccc	ata	agt	cct	att	gaa	act	gta	cca	gta	aga	cta	aaa	336
Leu	Asn	Phe	Pro	Ile	Ser	Pro	Ile	Glu	Thr	Val	Pro	Val	Arg	Leu	Lys	
			100					105					110			
cca	gga	atg	gat	ggg	cca	aaa	gtt	aag	caa	tgg	cca	cta	aca	gaa	gaa	384
Pro	Gly	Met	Asp	Gly	Pro	Lys	Val	Lys	Gln	Trp	Pro	Leu	Thr	Glu	Glu	
		115					120					125				
aaa	atc	aaa	gca	ttg	ata	gaa	att	tgt	aca	gaa	atg	gaa	aag	gaa	gga	432
Lys	Ile	Lys	Ala	Leu	Ile	Glu	Ile	Cys	Thr	Glu	Met	Glu	Lys	Glu	Gly	
	130					135					140					
aaa	att	gaa	aaa	att	ggg	cct	gaa	aat	cca	tac	aat	act	cca	gta	ttt	480
Lys	Ile	Glu	Lys	Ile	Gly	Pro	Glu	Asn	Pro	Tyr	Asn	Thr	Pro	Val	Phe	
145					150					155					160	
gcc	ata	agg	aaa	aaa	gac	agt	act	aaa	tgg	aga	aaa	tta	gta	gat	ttc	528
Ala	Ile	Arg	Lys	Lys	Asp	Ser	Thr	Lys	Trp	Arg	Lys	Leu	Val	Asp	Phe	
				165					170					175		
aga	gaa	ctt	aat	aag	aga	act	caa	gac	ttt	tgg	gaa	att	caa	tta	gga	576
Arg	Glu	Leu	Asn	Lys	Arg	Thr	Gln	Asp	Phe	Trp	Glu	Ile	Gln	Leu	Gly	
			180					185					190			
ata	cca	cat	ccc	gca	ggg	tta	aaa	aag	aaa	aaa	tca	gta	aca	gta	ctg	624
Ile	Pro	His	Pro	Ala	Gly	Leu	Lys	Lys	Lys	Lys	Ser	Val	Thr	Val	Leu	
		195					200					205				
gat	gtg	ggg	gat	gca	tat	ttt	tca	gtt	ccc	tta	gat	aaa	gac	ttc	agg	672
Asp	Val	Gly	Asp	Ala	Tyr	Phe	Ser	Val	Pro	Leu	Asp	Lys	Asp	Phe	Arg	
	210					215					220					
aag	tat	act	gca	ttt	acc	ata	cct	agt	gta	aat	aat	gag	aca	cca	gga	720
Lys	Tyr	Thr	Ala	Phe	Thr	Ile	Pro	Ser	Val	Asn	Asn	Glu	Thr	Pro	Gly	
225					230					235					240	

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att aga tat caa tac aat gtg ctt cca caa gga tgg aaa gga tca cca      768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
                245                250                255

gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa      816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys
                260                265                270

caa aat cca gaa yta gtt atc tac caa tac atg gat gat ttg tat gta      864
Gln Asn Pro Glu Xaa Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val
                275                280                285

gga tca gac tta gaa ata gar aag cat aga gca aaa ata gag gaa ctg      912
Gly Ser Asp Leu Glu Ile Glu Lys His Arg Ala Lys Ile Glu Glu Leu
                290                295                300

aga gaa cat ctg tya aaa tgg ggg ttt acc aca cca gac aaa aaa cat      960
Arg Glu His Leu Xaa Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His
                305                310                315                320

cag aaa gaa cct cca ttt ctt tgg atg ggt tat gaa ctc cat cct gat      1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
                325                330                335

aaa tgg aca gta cag acc ata aag ctg cca gaa aaa gac agc tgg act      1056
Lys Trp Thr Val Gln Thr Ile Lys Leu Pro Glu Lys Asp Ser Trp Thr
                340                345                350

gtc aat gat ata cag aag tta gtg gga aaa ttg aat tgg gca agt caa      1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
                355                360                365

att tat cca ggg
Ile Tyr Pro Gly
                370

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<210> 112
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

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<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

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<400> 112
cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly
  1                5                10                15

ggg cag cta aag gaa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
                20                25                30

tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atk ata ggg      144
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Xaa Ile Gly
                35                40                45

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gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ctt gta Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Leu Val 50 55 60	192
gaa att tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr 65 70 75 80	240
cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr 85 90 95	288
tta aat ttt ccc att agt cct att gag act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtc aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta atg gaa att tgt gca gaa wtg gaa aag gaa gga Lys Ile Lys Ala Leu Met Glu Ile Cys Ala Glu Xaa Glu Lys Glu Gly 130 135 140	432
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gcc ata aag aaa aaa gac agc act aaa tgg ara aaa tta gta gat ttc Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Xaa Lys Leu Val Asp Phe 165 170 175	528
aga gaa ctt aat aar aga act caa gac ttt tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta cta Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat gaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg 210 215 220	672
aag tat act gca ttt acc ata cct agt ata aac aat gag acm cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Xaa Pro Gly 225 230 235 240	720
att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agt agc atg aca aaa att tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gac ata gtt atc tat caa tac atg gat gat ttg tat gta Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300	912

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aga cag cat ctg ttg aag tgg gga ttk tmc aca cca gac aaa aaa cat      960
Arg Gln His Leu Leu Lys Trp Gly Xaa Xaa Thr Pro Asp Lys Lys His
305                      310                      315                      320

cag aaa saa cct cca ttc ctt tgg atg ggt tat gaa ctc cmt cct gat      1008
Gln Lys Xaa Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu Xaa Pro Asp
                      325                      330                      335

aaa tgg aca gta caa cct ata gtg ctg cca gaa aag gac agc tgg act      1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
                      340                      345                      350

gtc aat gac ata cag aag tta gtg gga aaa ttr aat tgg gca agt cag      1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Xaa Asn Trp Ala Ser Gln
                      355                      360                      365

att tac gca ggg
Ile Tyr Ala Gly
370

<210> 113
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

<400> 113
cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly
1                      5                      10                      15

ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
                      20                      25                      30

tta gaa gaa atg aat ttg cca gga aaa tgg aaa cca aaa atg ata ggg      144
Leu Glu Glu Met Asn Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly
                      35                      40                      45

gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ctc ata      192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Leu Ile
50                      55                      60

gaa atc tgt gga cat aaa act ata ggt aca gta tta ata gga cct aca      240
Glu Ile Cys Gly His Lys Thr Ile Gly Thr Val Leu Ile Gly Pro Thr
65                      70                      75                      80

cct gtc aac ata att gga aga aat ctg ttg act cag ctt ggt tgt act      288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr
                      85                      90                      95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag      336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
100                      105                      110

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cca gga atg gat ggt cca aga gtt aaa caa tgg cca ttg acm gaa gaa Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Xaa Glu Glu 115 120 125	384
aaa ata aaa gca tta ata gaa atc tgc aca gaa atg gaa aag gam sga Lys Ile Lys Ala Leu Ile Glu Ile Cys Thr Glu Met Glu Lys Xaa Xaa 130 135 140	432
waa att tca aaa mta ggg cct gam wat cca tac aat act cca gta ttt Xaa Ile Ser Lys Xaa Gly Pro Xaa Xaa Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528
aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cac ccg gca ggg tta aaa aag aac aaa tca gta aca gtg ttg Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gag ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Glu Phe Arg 210 215 220	672
aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240	720
atc aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa tst agc atg aca aaa atc tta gag cct ttt aga aaa Ala Ile Phe Gln Xaa Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gaa ata gtt atc tgt caa tac atg gat gat ttg tat gta Gln Asn Pro Glu Ile Val Ile Cys Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ttg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300	912
aga gaa cat ctg ttg aag tgg gga ttt acc aca cca gat aaa aaa cat Arg Glu His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His 305 310 315 320	960
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gag ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056
gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104

att tat gca ggg
 ile tyr ala gly
 370

1116

<210> 114
 <211> 1116
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)

<220>
 <221> CDS
 <222> (1)...(297)
 <223> HIV Protease

<221> CDS
 <222> (298)...(1116)
 <223> Portion of HIV Reverse Transcriptase

<400> 114
 cmt caa atm amt ctt tgg car mra ccc cta gtc cna awn nmm gkk agg 48
 Xaa Gln Xaa Xaa Leu Trp Gln Xaa Pro Leu Val Xaa Xaa Xaa Xaa Arg
 1 5 10 15
 ggg gca aat aag gaa gct cta tta gac aca gga gca gat gat mca gta 96
 Gly Ala Asn Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Xaa Val
 20 25 30
 tta gaa gaa atg wat tta cca gga aaa tgg aaa cca aaa atg ata ggg 144
 Leu Glu Glu Met Xaa Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly
 35 40 45
 gga att gga ggt ttt atc aaa gta agn cag tat gag cag ata ccc ata 192
 Gly Ile Gly Gly Phe Ile Lys Val Xaa Gln Tyr Glu Gln Ile Pro Ile
 50 55 60
 gaa atc tgt gga cat aaa gct ata ggt aca gta ttg gta ggm cct aca 240
 Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Xaa Pro Thr
 65 70 75 80
 cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act 288
 Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
 85 90 95
 tta aat ttt ccc att agt cct att gaa act gta cca gtg aaa tta aag 336
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
 100 105 110
 cca gga atg gat ggc cca aaa gtt aaa caa tgg cca tta aca gaa gaa 384
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
 115 120 125
 aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aaa gaa ggg 432
 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
 130 135 140
 aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt 480
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
 145 150 155 160
 gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc 528
 Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
 165 170 175

```

aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtc caa tta gga      576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
      180                               185                               190

ata cca cat cct gca ggg tta aaa aag aaa aaa tca gta aca gtg ctg      624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu
      195                               200                               205

gac gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg      672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg
      210                               215                               220

aag tat act gca ttt tcy ata cct agt aca aac aat gag aca cca ggg      720
Lys Tyr Thr Ala Phe Xaa Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly
      225                               230                               235                               240

agt agg tat caa tac aat gtg ctt cca cag gga tgg aaa gga tca cca      768
Ser Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
      245                               250                               255

gca ata ttc caa agt agc atg ata aaa atc tta gag cct ttt aga aaa      816
Ala Ile Phe Gln Ser Ser Met Ile Lys Ile Leu Glu Pro Phe Arg Lys
      260                               265                               270

caa aat cca raa att gtg atc tat cma tac mtg gat gat ttg tat gta      864
Gln Asn Pro Xaa Ile Val Ile Tyr Xaa Tyr Xaa Asp Asp Leu Tyr Val
      275                               280                               285

gga tct gac tta gaa ata gaa cag cat aga aca aaa ata gag gaa ctg      912
Gly Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Glu Glu Leu
      290                               295                               300

aga caa cat ctg ttg agg tgg gga ttt acc aca cca gac aag aaa cat      960
Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His
      305                               310                               315                               320

cag aar gaa cct ccg ttc ctt tgg atg ggt tat gaa ctc cat cct gat      1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
      325                               330                               335

aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac ags ttg rct      1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Xaa Leu Xaa
      340                               345                               350

kca aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag      1104
Xaa Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
      355                               360                               365

att tac tca ggg
Ile Tyr Ser Gly
      370

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<210> 115

<211> 1116

<212> DNA

<213> Human Immunodeficiency Virus (HIV)

<220>

<221> CDS

<222> (1) ... (297)

<223> HIV Protease

<221> CDS

<222> (298)...(1116)

<223> Portion of HIV Reverse Transcriptase

<400> 115

cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata aag ata ggg	48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly	
1 5 10 15	
ggg cag cta aag gaa gct cta ata gat aca gga gca gat gat aca gtg	96
Gly Gln Leu Lys Glu Ala Leu Ile Asp Thr Gly Ala Asp Asp Thr Val	
20 25 30	
tta gaa gaa atg agt ata cca gga aaa tgg aaa cca aaa ttg ata ggg	144
Leu Glu Glu Met Ser Ile Pro Gly Lys Trp Lys Pro Lys Leu Ile Gly	
35 40 45	
gga att gga ggt ttt atc aaa gta aga cag tat gat cag gkg ccc gta	192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Xaa Pro Val	
50 55 60	
gaa att tgt gga cat aaa gct ata ggt mca gtw tta ata ggm cct aca	240
Glu Ile Cys Gly His Lys Ala Ile Gly Xaa Xaa Leu Ile Xaa Pro Thr	
65 70 75 80	
cct gcc aac ata att gga agg aat ctg ttg act cag att ggt tgc act	288
Pro Ala Asn Ile Ile Gly Arg Asn Leu Thr Gln Ile Gly Cys Thr	
85 90 95	
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag	336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys	
100 105 110	
cca gga atg gat ggc cca aaa gtt aag caa tgg cca ttg aca gaa gag	384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu	
115 120 125	
aaa ata aaa gca tta aca gaa att tgt aca gaa atg gaa aag gaa gga	432
Lys Ile Lys Ala Leu Thr Glu Ile Cys Thr Glu Met Glu Lys Glu Gly	
130 135 140	
aag att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt	480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe	
145 150 155 160	
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc	528
Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe	
165 170 175	
aga gaa ctt aat aag aga act caa gat ttc tgg gaa gtt caa tta gga	576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly	
180 185 190	
ata cca cat cct gca ggg tta aaa aag aaa aaa tca gta aca gta ctg	624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu	
195 200 205	
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat gaa gac ttt agg	672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg	
210 215 220	
aaa tat act gca ttt acc ata cct agt gta aac aat gag aca cca ggg	720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Val Asn Asn Glu Thr Pro Gly	
225 230 235 240	

att aga tat cag tat aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa tgt agt atg aca aaa ata tta gag ccc ttt aga aaa Ala Ile Phe Gln Cys Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gac cta gtt atc tat caa tac gtg gat gat ttg tat gta Gln Asn Pro Asp Leu Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300	912
aga caa cat ctg ttg aaa tgg ggt ttt acc aca cca gac aaa aag cat Arg Gln His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His 305 310 315 320	960
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cca gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056
gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
att tac cca ggg Ile Tyr Pro Gly 370	1116

<210> 116
 <211> 1116
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)

<220>
 <221> CDS
 <222> (1)...(297)
 <223> HIV Protease

<221> CDS
 <222> (298)...(1116)
 <223> Portion of HIV Reverse Transcriptase

<400> 116 cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata aag ata ggg Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly 1 5 10 15	48
ggg cag cta aag gaa gct cta tta gat aca gga gca gat gac aca gta Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30	96
tta gaa gaa ata agt ctg cca gga aga tgg aaa cca aaa ttg ata ggg Leu Glu Glu Ile Ser Leu Pro Gly Arg Trp Lys Pro Lys Leu Ile Gly 35 40 45	144

gga att gga ggt ttt atc aaa gta aag cag tat gat cag ata ccc ata 192
 Gly Ile Gly Gly Phe Ile Lys Val Lys Gln Tyr Asp Gln Ile Pro Ile
 50 55 60

gaa atc tgt gga cat aaa gct ata ggt aca gta tta gta ggm cct aca 240
 Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Xaa Pro Thr
 65 70 75 80

cct gtc aac ata gtt gga aga aat ctg ttg act cag ctt ggt tgc act 288
 Pro Val Asn Ile Val Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr
 85 90 95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
 100 105 110

cca gga atg gat ggc cca aag gtt aag caa tgg cca ttg aca gaa gaa 384
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
 115 120 125

aaa ata aaa gca tta gta gaa att tgt aca gaa ttg gaa aag gaa ggg 432
 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Lys Glu Gly
 130 135 140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt 480
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
 145 150 155 160

gcc ata aag aaa aaa gac agt aca aaa tgg aga aaa tta gta gat ttc 528
 Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
 165 170 175

aga gaa ctt aat aag aga act caa gac ttt tgg gaa gtt caa cta ggg 576
 Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
 180 185 190

ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta ctg 624
 Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu
 195 200 205

gat gtg ggt gat gca tat ttt tca gtt ccc ttg gat aaa gac ttc agg 672
 Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg
 210 215 220

aag tac act gca ttt acc ata cct agt ata aat aat gag aca cca ggg 720
 Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly
 225 230 235 240

att aga tat caa tac aat gtg ctt cca cag gga tgg aaa gga tca cca 768
 Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
 245 250 255

gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa 816
 Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys
 260 265 270

caa aat cca gac ata gtt atc tat caa tac gta gat gac ttg tat gta 864
 Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val
 275 280 285

gga tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg 912
 Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu
 290 295 300

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aga caa cat ctg tgg aag tgg ggg ttt tac aca cca gat aaa aaa cat      960
Arg Gln His Leu Trp Lys Trp Gly Phe Tyr Thr Pro Asp Lys Lys His
305                      310                      315                      320

cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat      1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
                      325                      330                      335

aaa tgg aca gta cag cct ata gtg ctg cca gaa aag gac agc tgg act      1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
                      340                      345                      350

gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt cag      1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
                      355                      360                      365

att tac cca ggg
Ile Tyr Pro Gly
                      370

<210> 117
<211> 1119
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1119)
<223> Portion of HIV Reverse Transcriptase

<400> 117
cct caa atc act ctt tgg caa cga ccc atc gtc aca ata aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Ile Gly
1                      5                      10                      15

ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
                      20                      25                      30

tta gaa gaa atg gat ttg cca gga aga tgg aca cca aaa atg ata ggg      144
Leu Glu Glu Met Asp Leu Pro Gly Arg Trp Thr Pro Lys Met Ile Gly
                      35                      40                      45

gga att gga ggt ctt gtc aaa gta aga cag tat gat cag ata ccc ata      192
Gly Ile Gly Gly Leu Val Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile
50                      55                      60

gaa atc tgt gga cat aaa act ata ggt aca gta tta gta gga cct aca      240
Glu Ile Cys Gly His Lys Thr Ile Gly Thr Val Leu Val Gly Pro Thr
65                      70                      75                      80

cct gcc aac ata att gga aga aat ctg ttg act cag ctt ggt tgt act      288
Pro Ala Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr
                      85                      90                      95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag      336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
100                      105                      110

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cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta gta gaa att tgt aca gaa ttg gaa aag gaa gga Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly 130 135 140	432
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gtg ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528
aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat cct gca gga tta aaa aag aaa aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gac aag gac ttt agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg 210 215 220	672
aaa tat act gca ttt acc ata cct agt aca aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly 225 230 235 240	720
att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agc agc atg aca aaa atc tta gat cct ttt aga aag Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Asp Pro Phe Arg Lys 260 265 270	816
caa aat cca gac ata gtt atc tgt caa tac atg gat gat ttg tat gta Gln Asn Pro Asp Ile Val Ile Cys Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300	912
aga gaa cat ctg tgg aag tgg ggg ttt tac aca cca gac aaa aaa cat Arg Glu His Leu Trp Lys Trp Gly Phe Tyr Thr Pro Asp Lys Lys His 305 310 315 320	960
cag aaa gaa cct ccg ttc ctc tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056
gtc aat gac ata cag aag tta gtg gga aaa ttg aac tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104

att tat yca ggg att
 Ile Tyr Xaa Gly Ile
 370

1119

<210> 118
 <211> 979
 <212> PRT
 <213> Human Immunodeficiency Virus

<400> 118
 Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys Pro Gly Met
 1 5 10 15
 Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu Lys Ile Lys
 20 25 30
 Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly Lys Ile Ser
 35 40 45
 Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe Ala Ile Lys
 50 55 60
 Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe Arg Glu Leu
 65 70 75 80
 Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly Ile Pro His
 85 90 95
 Pro Ala Gly Leu Lys Gln Lys Lys Ser Val Thr Ile Leu Asp Val Gly
 100 105 110
 Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Gly Phe Arg Lys Tyr Thr
 115 120 125
 Ala Phe Thr Ile Pro Ser Arg Asn Asn Glu Thr Pro Gly Ile Arg Tyr
 130 135 140
 Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro Ala Ile Phe
 145 150 155 160
 Gln Ser Ser Met Thr Arg Ile Leu Glu Pro Phe Arg Lys Gln Asn Pro
 165 170 175
 Glu Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val Gly Ser Asp
 180 185 190
 Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Leu Arg Gly His
 195 200 205
 Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His Gln Lys Glu
 210 215 220
 Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp Lys Trp Thr
 225 230 235 240
 Val Gln Pro Ile Lys Leu Pro Glu Lys Asp Ser Trp Thr Val Asn Asp
 245 250 255
 Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln Ile Tyr Ala
 260 265 270
 Gly Ile Lys Val Arg Gln Leu Cys Lys Leu Leu Arg Gly Thr Lys Ala
 275 280 285
 Leu Thr Glu Val Ile Pro Leu Thr Glu Glu Ala Glu Leu Glu Leu Ala
 290 295 300
 Glu Asn Arg Glu Ile Leu Lys Glu Pro Val His Gly Val Tyr Tyr Asp
 305 310 315 320
 Pro Ser Lys Asp Leu Ile Ala Glu Ile Gln Lys Gln Gly Gln Gly Gln
 325 330 335
 Trp Thr Tyr Gln Ile Tyr Gln Glu Pro Phe Lys Asn Leu Lys Thr Gly
 340 345 350
 Lys Tyr Ala Arg Met Arg Gly Ala His Thr Asn Asp Val Lys Gln Leu
 355 360 365
 Thr Glu Ala Val Gln Lys Ile Thr Thr Glu Ser Ile Val Ile Trp Gly
 370 375 380
 Lys Thr Pro Lys Phe Lys Leu Pro Ile Gln Lys Glu Thr Trp Glu Thr
 385 390 395 400
 Trp Trp Thr Glu Tyr Trp Gln Ala Thr Trp Ile Pro Glu Trp Glu Phe
 405 410 415

Val	Asn	Thr	Pro	Pro	Leu	Val	Lys	Leu	Trp	Tyr	Gln	Leu	Glu	Lys	Glu
			420					425					430		
Pro	Ile	Val	Gly	Ala	Glu	Thr	Phe	Tyr	Val	Asp	Gly	Ala	Ala	Asn	Arg
		435					440					445			
Glu	Thr	Lys	Leu	Gly	Lys	Ala	Gly	Tyr	Val	Thr	Asn	Arg	Gly	Arg	Gln
	450					455					460				
Lys	Val	Val	Thr	Leu	Thr	Asp	Thr	Thr	Asn	Gln	Lys	Thr	Glu	Leu	Gln
465					470					475					480
Ala	Ile	Tyr	Leu	Ala	Leu	Gln	Asp	Ser	Gly	Leu	Glu	Val	Asn	Ile	Val
			485						490					495	
Thr	Asp	Ser	Gln	Tyr	Ala	Leu	Gly	Ile	Ile	Gln	Ala	Gln	Pro	Asp	Gln
			500					505					510		
Ser	Glu	Ser	Glu	Leu	Val	Asn	Gln	Ile	Ile	Glu	Gln	Leu	Ile	Lys	Lys
		515					520					525			
Glu	Lys	Val	Tyr	Leu	Ala	Trp	Val	Pro	Ala	His	Lys	Gly	Ile	Gly	Ser
	530					535					540				
Pro	Ile	Glu	Thr	Val	Pro	Val	Lys	Leu	Lys	Pro	Gly	Met	Asp	Gly	Pro
545					550					555					560
Lys	Val	Lys	Gln	Trp	Pro	Leu	Thr	Glu	Glu	Lys	Ile	Lys	Ala	Leu	Val
			565					570						575	
Glu	Ile	Cys	Thr	Glu	Met	Glu	Lys	Glu	Gly	Lys	Ile	Ser	Lys	Ile	Gly
			580					585					590		
Pro	Glu	Asn	Pro	Tyr	Asn	Thr	Pro	Ile	Phe	Ala	Ile	Lys	Lys	Lys	Asp
		595					600					605			
Ser	Thr	Lys	Trp	Arg	Lys	Leu	Val	Asp	Phe	Arg	Glu	Leu	Asn	Lys	Arg
	610					615					620				
Thr	Gln	Asp	Phe	Trp	Glu	Val	Gln	Leu	Gly	Ile	Pro	His	Pro	Ala	Gly
625					630					635					640
Leu	Lys	Gln	Lys	Lys	Ser	Val	Thr	Ile	Leu	Asp	Val	Gly	Asp	Ala	Tyr
			645						650					655	
Phe	Ser	Val	Pro	Leu	Asp	Glu	Gly	Phe	Arg	Lys	Tyr	Thr	Ala	Phe	Thr
			660					665					670		
Ile	Pro	Ser	Arg	Asn	Asn	Glu	Thr	Pro	Gly	Ile	Arg	Tyr	Gln	Tyr	Asn
		675					680					685			
Val	Leu	Pro	Gln	Gly	Trp	Lys	Gly	Ser	Pro	Ala	Ile	Phe	Gln	Ser	Ser
	690					695					700				
Met	Thr	Arg	Ile	Leu	Glu	Pro	Phe	Arg	Lys	Gln	Asn	Pro	Glu	Ile	Val
705					710					715					720
Ile	Tyr	Gln	Tyr	Met	Asp	Asp	Leu	Tyr	Val	Gly	Ser	Asp	Leu	Glu	Ile
			725						730					735	
Gly	Gln	His	Arg	Ala	Lys	Ile	Glu	Glu	Leu	Arg	Gly	His	Leu	Leu	Lys
			740					745					750		
Trp	Gly	Phe	Thr	Thr	Pro	Asp	Lys	Lys	His	Gln	Lys	Glu	Pro	Pro	Phe
		755					760					765			
Leu	Trp	Met	Gly	Tyr	Glu	Leu	His	Pro	Asp	Lys	Trp	Thr	Val	Gln	Pro
	770					775					780				
Ile	Lys	Leu	Pro	Glu	Lys	Asp	Ser	Trp	Thr	Val	Asn	Asp	Ile	Gln	Lys
785					790					795					800
Leu	Val	Gly	Lys	Leu	Asn	Trp	Ala	Ser	Gln	Ile	Tyr	Ala	Gly	Ile	Lys
			805						810					815	
Val	Arg	Gln	Leu	Cys	Lys	Leu	Leu	Arg	Gly	Thr	Lys	Ala	Leu	Thr	Glu
			820					825					830		
Val	Ile	Pro	Leu	Thr	Glu	Glu	Ala	Glu	Leu	Glu	Leu	Ala	Glu	Asn	Arg
		835					840					845			
Glu	Ile	Leu	Lys	Glu	Pro	Val	His	Gly	Val	Tyr	Tyr	Asp	Pro	Ser	Lys
	850					855					860				
Asp	Leu	Ile	Ala	Glu	Ile	Gln	Lys	Gln	Gly	Gln	Gly	Gln	Trp	Thr	Tyr
865					870					875					880
Gln	Ile	Tyr	Gln	Glu	Pro	Phe	Lys	Asn	Leu	Lys	Thr	Gly	Lys	Tyr	Ala
			885						890					895	
Arg	Met	Arg	Gly	Ala	His	Thr	Asn	Asp	Val	Lys	Gln	Leu	Thr	Glu	Ala
			900					905					910		
Val	Gln	Lys	Ile	Thr	Thr	Glu	Ser	Ile	Val	Ile	Trp	Gly	Lys	Thr	Pro
		915					920					925			

Lys	Phe	Lys	Leu	Pro	Ile	Gln	Lys	Glu	Thr	Trp	Glu	Thr	Trp	Trp	Thr
	930					935					940				
Glu	Tyr	Trp	Gln	Ala	Thr	Trp	Ile	Pro	Glu	Trp	Glu	Phe	Val	Asn	Thr
945					950					955					960
Pro	Pro	Leu	Val	Lys	Leu	Trp	Tyr	Gln	Leu	Glu	Lys	Glu	Pro	Ile	Val
				965					970					975	
Gly	Ala	Glu													